

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:46:23 ; Search time 138.474 Seconds
(without alignments)

463.258 Million cell updates/sec

Title: US-10-623-189-1

Perfect score: 736

Sequence: 1 VPQKVQDRTKLIKTIIVTR.....SRQQSLQDMLWQLDLSPGC 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	146	2 AAW00013	Aaw00013 Acid stab
2	736	100.0	146	2 AAR99490	Aar99490 Chimeric
3	736	100.0	146	2 AAW00539	Aaw00539 Human mat
4	736	100.0	146	2 AAW30892	Aaw30892 Synthetic
5	736	100.0	146	2 AAW34482	Aaw34482 Human obe
6	736	100.0	146	2 AAW10151	Aaw10151 Properly
7	736	100.0	146	2 AAW22901	Aaw22901 Biologica
8	736	100.0	146	2 AAW30791	Aaw30791 Obesity p
9	736	100.0	146	2 AAW26194	Aaw26194 Obesity p
10	736	100.0	146	2 AAW34483	Aaw34483 Human obe
11	736	100.0	146	2 AAW32575	Aaw32575 Anti obes
12	736	100.0	146	2 AAW34489	Aaw34489 Obesity p
13	736	100.0	146	2 AAW69682	Aaw69682 Human obe
14	736	100.0	146	2 AAW53342	Aaw53342 Obesity p
15	736	100.0	146	2 AAY43311	Aay43311 Human lep
16	736	100.0	146	2 AAY06102	Aay06102 Mature obe
17	736	100.0	146	3 AAY92712	Aay92712 Mature le
18	736	100.0	146	3 AAY82111	Aay82111 Mature hu
19	736	100.0	146	3 AAY80260	Aay80260 Human mat
20	736	100.0	146	3 AAY83768	Aay83768 Human OB
21	736	100.0	146	3 AAY97871	Aay97871 Mature wi
22	736	100.0	146	3 AAY95786	Aay95786 Mature re
23	736	100.0	146	3 AAY95531	Aay95531 Human mat
24	736	100.0	146	3 AAB14265	Aab14265 Mature hu

25	736	100.0	146	4 AAB70130	Aab70130 Mature hu
26	736	100.0	146	5 AAE23614	Aae23614 Human lep
27	736	100.0	146	5 ABG32264	Abg32264 Recombina
28	736	100.0	146	5 ABP63579	Abp63579 Human obe
29	736	100.0	146	5 ADG65529	Adg65529 Human lep
30	736	100.0	146	5 ABR57162	AbR57162 Recombina
31	736	100.0	146	7 ADC06694	Adc06694 Leptin ta
32	736	100.0	146	7 ADD26675	Add26675 Human adi
33	736	100.0	146	7 ADD71107	Add71107 Human lep
34	736	100.0	146	8 ADL80474	Adl80474 Mature hu
35	736	100.0	146	8 ADL88877	Adl88877 Human cyt
36	736	100.0	146	9 ADV90297	Adv90297 Protease-
37	736	100.0	146	9 ADW96956	Adw96956 Human wil
38	736	100.0	147	2 AAW34394	Aaw34394 Human met
39	736	100.0	147	2 AAW27167	Aaw27167 Human rec
40	736	100.0	147	2 AAW53328	Aaw53328 Human obe
41	736	100.0	147	2 AAY43314	Aay43314 Human lep
42	736	100.0	147	3 AAY92261	Aay92261 Mature re
43	736	100.0	148	2 AAW07192	Aaw07192 Human ant
44	736	100.0	148	2 AAW28801	Aaw28801 Human mas
45	736	100.0	148	2 AAW71849	Aaw71849 Obesity p

ALIGNMENTS

RESULT 1
AAW00013
ID AAW00013 standard; protein; 146 AA.
AC AAW00013;
DT 30-SEP-1996 (first entry)
DE Acid stable modified ob protein (Asp22Aan).
XX
KW ob protein; adiposity regulating hormone; mouse; acid stability;
KW adsorption characteristic; obesity; type II diabetes;
KW cardiovascular disease; cancer.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 22
FT Disulfide-bond 96..146
XX
FN EP725078-A1.
XX
PD 07-AUG-1996.
XX
PF 29-JAN-1996; 96EP-00300612.
XX
PR 31-JAN-1995; 95US-00381048.
XX
PR 06-FEB-1995; 95US-00383638.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Basinsky MB, Dimarchi RD, Heath WP, Schonher BE;
XX
XX WPI; 1996-356062/36.
XX
XX Mammalian derived anti-obesity proteins which regulate fat tissue - used
XX for treating obesity and to reduce risk for type II diabetes,
XX cardiovascular disease and cancer.
XX
XX Example 4; Page 19; 42pp; English.
XX
XX This sequence represents a modified ob proteins. ob proteins are thought
XX to be adiposity regulating hormones. This sequence is based on the mouse
XX ob protein sequence. Proteins such as this have improved stability, esp.
XX acid stability, and improved adsorption characteristics compared to the
XX wild type protein disclosed in Yiying Zhang et al, Nature 372: 425-32

CC (December 194). These proteins correspond to the generic formulae given
 CC in AAR99497-98). They are biologically active for the treatment of
 CC obesity. Individuals treated with these proteins have a reduced risk for
 CC type II diabetes, cardiovascular disease and cancer

XX Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
 |||||
 Db 1 VPIQKQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
 |||||
 QY 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 120
 |||||
 Db 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 120
 |||||
 QY 121 TEVVALSRQGSLOQMLWQLDLSPGC 146
 |||||
 Db 121 TEVVALSRQGSLOQMLWQLDLSPGC 146
 |||||

RESULT 2

AAR99490
 ID AAR99490 standard; protein; 146 AA.

XX AAR99490;

AC AAR99490;

DT 16-OCT-2003 (revised)

DT 26-SEP-1996 (first entry)

XX Chimeric ob protein.

XX ob protein; human; substitution; murine; mouse; obesity; stability;

XX type II diabetes; cardiovascular disease; cancer.

XX Mus musculus.

XX Homo sapiens.

XX Chimeric.

Key Location/Qualifiers

FT Misc-difference 22 /note= "Opt. Gln or Asp"

FT Misc-difference 27 /note= "Opt. Ala"

FT Misc-difference 28 /note= "Opt. Glu or absent"

FT Misc-difference 54 /note= "Opt. Ala"

FT Misc-difference 68 /note= "Opt. Leu"

FT Misc-difference 72 /note= "Opt. Glu or Asp"

FT Misc-difference 77 /note= "Opt. Ala"

FT Disulfide-bond 96. .146

FT Misc-difference 97 /note= "Opt. replaced with Gln, Asn, Ala, Gly, Ser or Pro"

FT Misc-difference 100 /note= "Opt. replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"

FT Misc-difference 101 /note= "Opt. replaced with Ser, Asn, Gly, His, Pro, Thr or Val"

FT Misc-difference 102 /note= "Opt. replaced with Arg"

FT Misc-difference 103 /note= "Opt. replaced with Ala"

FT Misc-difference 105 /note= "Opt. replaced with Gln"

FT Misc-difference 106 /note= "Opt. replaced with Lys or Ser"
 FT Misc-difference 107 /note= "Opt. replaced with Pro"
 FT Misc-difference 108 /note= "Opt. replaced with Glu"
 FT Misc-difference 111 /note= "Opt. replaced with Asp"
 FT Misc-difference 118 /note= "Opt. Leu"
 FT Misc-difference 138 /note= "Opt. replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"

XX EP725079-AL.

XX 07-AUG-1996.

XX 29-JAN-1996; 96BP-00300613.

XX 31-JAN-1995; 95US-00381048.

XX 06-FEB-1995; 95US-00383638.

XX 22-JUN-1995; 95US-0000450P.

XX 11-AUG-1995; 95US-0002161P.

XX (ELIL) LILLY & CO ELI.

XX Basinski MB, Dimarchi RD, Flora DB, Hale JE, Heath WF;

XX Hoffmann JA, Schoner BE;

XX WPI; 1996-356063/36.

XX N-PSDB; AAT34254.

XX Modified human anti-obesity proteins which regulate fat tissue - have

XX increased stability, for treating obesity and to reduce risk for type II

XX diabetes, cardiovascular disease and cancer.

XX Claim 3; Page 47; 56pp; English.

XX The sequences given in AAR99490-96 represent modified ob proteins which
 CC are based on the human ob protein sequence. These protein sequences are
 CC covered by the generic sequence given in AAR99489. In these proteins,
 CC specific amino acids are substituted for the residues found in the
 CC corresponding positions in murine ob protein. These proteins are
 CC biologically active for the treatment of obesity, and are more stable
 CC than either the murine or human proteins. Individuals treated with these
 CC proteins have a reduced risk for type II diabetes, cardiovascular disease
 CC and cancer. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
 |||||

Db 1 VPIQKQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
 |||||

QY 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 120
 |||||

Db 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFSKSLPWSAGLETLDLSLGGVLEASGYS 120
 |||||

QY 121 TEVVALSRQGSLOQMLWQLDLSPGC 146
 |||||

Db 121 TEVVALSRQGSLOQMLWQLDLSPGC 146
 |||||

RESULT 3

AAW00539

ID AAW00539 standard; protein; 146 AA.

XX AAW00539;

XX 13-SEP-1996 (first entry)
DT Human mature obesity protein.
DE
XX Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
KW food intake; energy expenditure; high blood pressure; cholesterol; human;
KW gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.
XX
OS Homo sapiens.
XX GB2292382-A.
PN
XX 21-FEB-1996.
PD
XX 17-AUG-1995; 95GB-00016947.
XX
XX 17-AUG-1994; 94US-00292345.
PR 30-NOV-1994; 94US-00347563.
PR 10-MAY-1995; 95US-00438431.
PR 07-JUN-1995; 95US-00483211.
XX (UVRQ) UNIV ROCKEFELLER.
PA
XX Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;
PI Burley SK;
PI
XX MPI; 1996-099009/11.
DR
XX Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
XX reducing wt. in treatment of diabetes, high blood pressure and high
PT cholesterol and for cosmetic reasons.
PT
XX
PS Claim 11; Page 7; 304pp; English.
XX
XX AAW0538-W00541 represent the mature proteins of the murine and human
CC obesity polypeptides (OBP) (full length sequences represented by AAR92719
CC and AAR92720). OBP (also known as leptin) is a hormone involved in the
CC regulation of body weight. This sequence has effects on both food intake
CC and energy expenditure. OBP and its analogues are useful for modifying
CC body weight (optionally combined with known medicaments), for treating
CC diabetes, high blood pressure or high cholesterol. The DNA encoding this
CC sequence (and sequences complementary to it) can be used in gene therapy
CC for modifying body weight. This protein can be used for reducing weight
CC for health or cosmetic reasons in obese humans, or to produce leaner food
CC animals. Antagonists of OBP (including antibodies) are useful for
CC increasing body weight, e.g. for treating weight loss associated with
CC cancer, or for cosmetic reasons in humans, or for production of Kobe beef
CC or Foie gras in domestic animals. OBP antibodies (Ab) can also be used in
CC diagnostic immunoassays for the presence of OBP. The formation of Ab-OBP
CC complexes enables in vitro evaluation of levels of OBP in a sample,
CC especially to detect diseases associated with elevated or decreased
CC levels, and to monitor treatment of these diseases
XX
SQ Sequence 146 AA;
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKQDDTKTLIKTVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKQDDTKTLIKTVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
Qy 121 TEVALSRQSLQDMLWQLDLSFGC 146
Db 121 TEVALSRQSLQDMLWQLDLSFGC 146
RESULT 5
AAW34482
ID AAW34482 standard; protein; 146 AA.
XX
AC AAW34482;
XX
DT 17-MAR-1998 (first entry)
XX
DE Human obesity protein.
XX
KW Obesity protein; therapy; obesity associated disorder; human.
OS Homo sapiens.

RESULT 4
AAW30892
ID AAW30892 standard; protein; 146 AA.
XX
AC AAW30892;
XX
DT 20-APR-1998 (first entry)
XX
DE Synthetic obesity protein.
XX
KW Obesity protein; sucrose; trehalose; treatment; obesity; diabetes;
KW cardiovascular disease; cancer.
XX
OS Synthetic.
XX
PN EP797999-A2.
XX
PD 01-OCT-1997.
XX
XX 24-MAR-1997; 97EP-00301995.
PR 26-MAR-1996; 96US-0014177P.
PR 05-APR-1996; 96US-0014951P.
XX (ELIL) LILLY & CO ELI.
XX
XX Beals JM, Edwards MJ, Pikal MJ, Rinella JV;
PI
XX MPI; 1997-472913/44.
DR
XX Pharmaceutical compositions comprising obesity protein - and sucrose
PT and/or trehalose.
PT
XX
PS Claim 2; Page 44; 48pp; English.
XX
CC A novel pharmaceutical composition comprises an obesity protein, e.g. the
CC present sequence, together with sucrose and/or trehalose. The composition
CC can be used to treat obesity and associated disorders, e.g. diabetes,
CC cardiovascular disease and cancer. The composition is stable and easy to
CC manufacture
XX
SQ Sequence 146 AA;
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKQDDTKTLIKTVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKQDDTKTLIKTVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
Qy 121 TEVALSRQSLQDMLWQLDLSFGC 146
Db 121 TEVALSRQSLQDMLWQLDLSFGC 146
RESULT 5
AAW34482
ID AAW34482 standard; protein; 146 AA.
XX
AC AAW34482;
XX
DT 17-MAR-1998 (first entry)
XX
DE Human obesity protein.
XX
KW Obesity protein; therapy; obesity associated disorder; human.
OS Homo sapiens.

XX EP784979-A2.
 PN
 XX
 PD 23-JUL-1997.
 XX
 PF 17-JAN-1997; 97EP-00300299.
 XX
 PR 19-JAN-1996; 96US-0010229P.
 PR 07-FEB-1996; 96GB-00002408.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 XX Beals JM, Dodd SW, Pekar AH;
 XX WPI; 1997-365736/34.
 DR
 XX
 XX New obesity protein compositions - comprising a soluble parenteral
 PT formulation containing a preservative selected from an alkyl:paraben and
 PT chloro:butanol.
 XX
 XX Disclosure; Page 6; 15pp; English.

XX This sequence represents the human obesity protein. It can be used in the
 CC formulation of the invention. The formulation of the invention is a
 CC soluble parenteral formulation that comprises an obesity protein and a
 CC preservative selected from an alkyl:paraben, chlorobutanol, or a mixture.
 CC The compositions can be used for treating obesity and disorders
 CC associated with obesity. In the formulations, the obesity protein remains
 CC stable and soluble at much higher concentrations and at a pH range
 CC acceptable for a soluble, parenteral formulation
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
 DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
 QY 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
 DB 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
 QY 121 TEVVALSRQGSIQDMLWQDLSPGC 146
 DB 121 TEVVALSRQGSIQDMLWQDLSPGC 146

RESULT 6
 AAW10151
 ID AAW10151 standard; protein; 146 AA.
 XX
 AC AAW10151;
 XX
 DT 27-AUG-2003 (revised)
 DT 02-OCT-1997 (first entry)
 XX Properly folded obesity protein intermediate.
 XX Intermediate; recombinant; production; obesity; regulation; fatty tissue;
 KW treatment; disease; diabetes; cardiovascular; cancer; properly folded.
 XX
 OS Mammalia.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= Val-P3
 FT /note= "R3 is absent, Met, Met-R4 or leader sequence
 FT (preferably Met-Arg, Gly-Ser-Pro or 1 of AAW08589-94),
 FT and R4 is any amino acid other than Pro"
 FT Modified-site 96

FT /note= "free Cys residue or part of mixed disulfide with,
 FT e.g. Cys, glutathione or 2-mercaptoethanol when Cys146 is
 FT free Cys residue"
 FT Modified-site 146
 FT /note= "free Cys residue or part of mixed disulfide with,
 FT e.g. Cys, glutathione or 2-mercaptoethanol when Cys96 is
 FT free Cys residue"
 PN W09700886-A1.
 XX
 XX 09-JAN-1997.
 XX
 XX 20-JUN-1996; 96WO-US010613.
 XX
 XX 22-JUN-1995; 95US-0000451P.
 XX (ELIL) LILLY & CO ELI.
 PA
 XX Hale JE, Mackellar W;
 XX WPI; 1997-087317/08.
 DR
 XX Properly folded intermediate for obesity protein - prepd. from inclusion
 PT bodies, provides high yield of active protein for treatment of obesity
 PT and its complications.
 XX
 PS Claim 1; Page 21; 66pp; English.

XX AAW10151 is a properly folded intermediate for the production of the
 CC biologically active obesity protein AAW22901, which has a similar
 CC structure but comprises a disulfide bridge between Cys96 and Cys146.
 CC AAW10151 is the final intermediate in the renaturation of a recombinant
 CC protein to AAW22901, which is an active anti-obesity protein for the
 CC regulation of fatty tissue and treatment of obesity related diseases,
 CC e.g. diabetes, cardiovascular disease and cancer. The production of
 CC AAW22901 via AAW10151 provides a high yield of active protein, and
 CC permits large scale manufacture with a high concentration of protein
 CC during the folding stage. AAW10151 already has the correct tertiary
 CC structure and conversion to AAW22901 is almost quantitative, with minimal
 CC formation of S-S linked dimers or multimers, negating the need for an
 CC aggregation preventing agent. AAW10151 is stable in the presence or
 CC absence of denaturant, is soluble in phosphate buffered saline and can be
 CC purified and characterised. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
 DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
 QY 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
 DB 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
 QY 121 TEVVALSRQGSIQDMLWQDLSPGC 146
 DB 121 TEVVALSRQGSIQDMLWQDLSPGC 146

RESULT 7
 AAW22901
 ID AAW22901 standard; protein; 146 AA.
 XX
 AC AAW22901;
 XX
 DT 27-AUG-2003 (revised)
 DT 02-OCT-1997 (first entry)
 XX Biologically active obesity protein.

XX Intermediate; recombinant; production; obesity; regulation; fatty tissue;
KW treatment; disease; diabetes; cardiovascular; cancer; properly folded.
XX Mammalia.
XX Key Location/Qualifiers
FH Modified-site 1 /label= Val-R3
FT /note= "R3 is absent, Met, Met-R4 or leader sequence
FT (preferably Met-Arg, Gly-Ser-Pro or 1 of AAW0589-94),
FT and R4 is any amino acid other than Pro"
FT Disulfide-bond 96. .146
XX WO9700886-A1.
XX 09-JAN-1997.
XX 20-JUN-1996; 96WO-US010613.
XX 22-JUN-1995; 95US-0000451P.
XX (ELIL) LILLY & CO ELI.
XX Hale JE, Mackellar W;
XX WPI; 1997-087317/08.
XX Properly folded intermediate for obesity protein - prep'd. from inclusion
PT bodies, provides high yield of active protein for treatment of obesity
PT and its complications.
XX Claim 12; Page 21; 66pp; English.

XX AAW10151 is a properly folded intermediate for the production of the
CC biologically active obesity protein AAW22901, which has a similar
CC structure but comprises a disulphide bridge between Cys96 and Cys146.
CC AAW10151 is the final intermediate in the renaturation of a recombinant
CC protein to AAW22901, which is an active anti-obesity protein for the
CC regulation of fatty tissue and treatment of obesity related diseases,
CC e.g. diabetes, cardiovascular disease and cancer. The production of
CC AAW22901 via AAW10151 provides a high yield of active protein, and
CC permits large scale manufacture with a high concentration of protein
CC during the folding stage. AAW10151 already has the correct tertiary
CC structure and conversion to AAW22901 is almost quantitative, with minimal
CC formation of S-S linked dimers or multimers, negating the need for an
CC aggregation preventing agent. AAW10151 is stable in the presence or
CC absence of denaturant, is soluble in phosphate buffered saline and can be
CC purified and characterised. (Updated on 27-AUG-2003 to correct OS field.)
XX Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
Qy 61 YQQLTSMPSRNVQISNDLENLRDLHLVLAFAFSKSCHLPWASGLETLDSLGLGVLEASGYS 120
Db 61 YQQLTSMPSRNVQISNDLENLRDLHLVLAFAFSKSCHLPWASGLETLDSLGLGVLEASGYS 120
Qy 121 TEVALSRLOGLSQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLSQDMLWQLDLSGPC 146

RESULT 8
AAW30791
ID AAW30791 standard; protein; 146 AA.
XX

AAW30791;
12-MAR-1998 (first entry)
Obesity protein complexed with a divalent metal cation.
Obesity protein; diabetes; cancer; cardiovascular disease;
divalent metal cation; leader sequence.
Homo sapiens.
Key Location/Qualifiers
FH Disulfide-bond 96. .146
XX WO9728824-A1.
XX 14-AUG-1997.
XX 24-JAN-1997; 97WO-US001188.
XX 06-FEB-1996; 96US-0011238P.
XX (ELIL) LILLY & CO ELI.
XX Hoffmann JA;
XX WPI; 1997-415077/38.
XX New compound comprising obesity protein and divalent metal cation - for
PT treatment of obesity and associated conditions, required at lower dose
PT than free protein.
XX Claim 3; Page 26; 33pp; English.
XX The present sequence represents a human obesity protein, which is
CC complexed with a divalent metal cation e.g. zinc and optionally has a
CC leader sequence. It is used to treat obesity and conditions (particularly
CC type II diabetes, cardiovascular disease and cancer) associated with it.
CC When formulated with the metal ion, it is more active, allowing reduction
CC in dose and thus reduction in cost and toxic side effects
XX Sequence 146 AA;
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
Qy 61 YQQLTSMPSRNVQISNDLENLRDLHLVLAFAFSKSCHLPWASGLETLDSLGLGVLEASGYS 120
Db 61 YQQLTSMPSRNVQISNDLENLRDLHLVLAFAFSKSCHLPWASGLETLDSLGLGVLEASGYS 120
Qy 121 TEVALSRLOGLSQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLSQDMLWQLDLSGPC 146
RESULT 9
AAW26194
ID AAW26194 standard; protein; 146 AA.
XX
AC AAW26194;
XX 18-FEB-1998 (first entry)
XX Obesity protein analogue #6.
XX Obesity protein analogue; divalent metal cation complex; therapy; cancer;
KW obesity; obesity associated disorder; diabetes; cardiovascular disease.
XX

RESULT 11
AAW32575
ID AAW32575 standard; protein; 146 AA.
XX
AC AAW32575;
XX
DT 22-JAN-1998 (first entry)
XX
DE Anti obesity protein analogue.
XX
KW Anti obesity protein analogue; neuropeptide Y; radiovascular; renal;
KW cerebral; central nervous system; CNS; heart; blood vessel;
KW sympathetic nerve; mouse; human; pain; nociception;
KW abnormal gastrointestinal motility; secretion;
KW abnormal drink intake disorder; abnormal food intake disorder;
KW sexual dysfunction; reproductive disorder; obesity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 96..146
XX
PN EP759441-A2.
XX
PD 26-FEB-1997.
XX
PF 26-JUN-1996; 96EP-00304723.
XX
PR 30-JUN-1995; 95US-0000740P.
PR 30-JUN-1995; 95US-0000752P.
PR 27-OCT-1995; 95US-0005910P.
PR 27-OCT-1995; 95US-0005911P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Bue-Valleskey JM, Heiman ML, Stephens TW, Tinsley FC;
XX
DR WPI; 1997-147497/14.
XX
FT New use of biologically active anti-obesity protein analogues - for
PT treating conditions associated with excess neuropeptide Y, e.g.
PT cardiovascular, renal, cerebral or CNS disorders.
XX
PS Claim 8; Page 84; 89pp; English.
XX
CC The present sequence represents an anti obesity protein analogue used in
CC the treatment or prevention of a condition associated with an excess of
CC neuropeptide Y. The protein analogue is useful in the treatment or
CC prevention of disorders or diseases pertaining to the heart, blood
CC vessels or the renal system, conditions related to increased sympathetic
CC nerve activity, cerebral diseases and diseases related to the central
CC nervous system, conditions related to pain or nociception, diseases
CC related to abnormal gastrointestinal motility and secretion, abnormal
CC drink and food intake disorders, diseases related to sexual dysfunction
CC and reproductive disorders, and conditions or disorders associated with
CC obesity. The protein analogue has improved properties due to its lower
CC isoelectric points and due to specific substitutions to the human obesity
CC protein. It is more stable than both the mouse and human obesity protein,
CC and is therefore superior therapeutic agents. It is more readily
CC formulated and stored
XX
SQ Sequence 146 AA;
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 9e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQVQDDTKLTIKTIYTRINDISHTQSVSKQVGTGLDTPGLHPILTLTKMDQTLAV 60
DB 1 VPIQVQDDTKLTIKTIYTRINDISHTQSVSKQVGTGLDTPGLHPILTLTKMDQTLAV 60
QY 61 YQQLTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

Db 61 YQQLTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
QY 121 TEVVVALSRLOGLQDMLWQLDLSPGC 146
Db 121 TEVVVALSRLOGLQDMLWQLDLSPGC 146
RESULT 12
AAW34489
ID AAW34489 standard; protein; 146 AA.
XX
AC AAW34489;
XX
DT 17-MAR-1998 (first entry)
XX
DE Obesity protein analogue #5.
XX
KW Obesity protein analogue; obesity associated disorder; therapy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 97 /note= "optionally replaced with Gln, Asn, Ala, Gly, Ser,
FT or Pro"
FT Misc-difference 100
FT Misc-difference 101 /note= "optionally replaced with Glu, Ala, Asp, Asn, Met,
FT Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu"
FT Misc-difference 102 /note= "optionally replaced with Ser, Asn, Gly, His, Pro,
FT Thr, or Val"
FT Misc-difference 103 /note= "optionally replaced with Arg"
FT Misc-difference 105 /note= "optionally replaced with Ala"
FT Misc-difference 106 /note= "optionally replaced with Gln"
FT Misc-difference 107 /note= "optionally replaced with Lys or Ser"
FT Misc-difference 108 /note= "optionally replaced with Pro"
FT Misc-difference 109 /note= "optionally replaced with Glu"
FT Misc-difference 111 /note= "optionally replaced with Asp"
FT Misc-difference 138 /note= "optionally replaced with Ala, Glu, Asp, Asn, Met,
FT Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu"
XX
PN EP784982-A2.
XX
PD 23-JUL-1997.
XX
PF 17-JAN-1997; 97EP-00300302.
XX
PR 19-JAN-1996; 96US-0010257P.
PR 07-FEB-1996; 96GB-00002409.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Beals JM, Dodd SW, Pekar AH;
XX
DR WPI; 1997-365738/34.
XX
FT New obesity protein analogue compositions - comprising a soluble
PT parenteral formulation containing a preservative selected from an
PT alkylparaben and chlorobutanol.
XX
PS Disclosure; Page 10; 46pp; English.
XX
CC This sequence represents an obesity protein analogue, and can be used in
CC the formulation of the invention. The formulation of the invention is a

CC soluble parenteral formulation that comprises an obesity protein analogue
CC and a preservative selected from an alkylparaben, chlorobutanol, or a
CC mixture. The compositions can be used for the treatment of obesity, or a
CC disorders associated with obesity. In the formulations, the obesity
CC protein analogue remains stable and soluble at much higher concentrations
CC and at a pH range acceptable for a soluble, multi-use parenteral
CC formulation

SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;

Best Local Similarity 100.0%; Pred. No. 9e-73; Score 150; DE query match 100.0%;

Matches	146;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVGTGLDFIPGLHPILTLSKMDQTLAV 60

Db 1 VPIQKVQDDTKLIKTI VTRINDISH TQSVSSKQKV TGLDFIPGLHPIL TLSKMDQTLAV 60

Qy 61 YQQILTSPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

Db 61 YQQILTSPSRNVQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

QY 121 TEVALSRLOGLQDMLWOLDLSPG 146

Db 121 TEVALSRQGSLODMLWOLDLSPGC 146

RESULT 13

AAW69682

ID AAW69682 standard; protein; 146 AA.

XX

AC AAW69682;

XX

DT 07-DEC-1998 (first entry)

DE Human obe

XX

KW Obesity protein; therapy; human.

XX

OS Homo sapiens.

XX

PN WO9831391-A1.

[illegible]

PD 23-JUL-1998.

XX DE 16 JAN 1968. 0850C UTC 0000Z

PP 16-JAN-1998;
YY

17-JAN-1997. 97JIS-0035714D

PK 17-OAN-1997; 97US-0033714F;
PR 07-AUG-1997; 97US-0054886P

XX
01-AUG-1991

PA (ELIL) LILLY & CO ELI.

XX
XX

PI Rinella JV;

XX XX

DR WPI; 1998-413818/35.

XX

Obesity protein soluble formulation for treating obesity - has pH greater than 8.0, at which aggregation of obesity proteins by preservatives is reduced allowing production of multi-use formulation.

XX

PS Disclosure; Page 11-12; 30pp; English.

XX

This is the amino acid sequence of human obesity protein. The invention discloses a stable, soluble formulation comprising an obesity protein and a preservative, and having a pH greater than 8.0. The obesity protein used in the formulation is preferably bio-synthesised in a host cell transformed with a recombinant DNA comprising a synthetic or semi-synthetic DNA encoding the protein. The soluble formulation can be administered to mammals to treat obesity (Claimed), especially humans when the obesity protein is human obesity protein. It was found that the physical stability of obesity proteins in the presence of preservatives such as phenol and cresol changes abruptly and is greatly enhanced at pH values above 8.0, such that the aggregation of obesity proteins caused by

PR 23-AUG-1996; 96US-0024121P.
 PR 23-AUG-1996; 96US-0025207P.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Beals JM, Rinella JV;
 XX
 DR WPI; 1998-180894/17.
 XX
 PT Parenteral obesity protein formulations - containing anionic amphiphilic
 PT solubiliser and stabiliser.
 XX
 PS Disclosure; Page 9; 45pp; English.
 XX
 CC The present sequence represents an obesity protein generic formula for
 CC producing obesity protein analogues for use in the present invention as
 CC part of a soluble parenteral formulation. The soluble parenteral
 CC formulations comprises an obesity protein or obesity protein analogue and
 CC an anionic amphiphilic compound. The formulations are used for treating
 CC obesity and associated disorders. The proteins are preferably present at
 CC a concentration of 5-50 mg/ml. The anionic amphiphilic compound
 CC solubilises and stabilises the protein
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSQKQVGTGLDFIPGLHPILTLKMDQTLAV 60
 Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSQKQVGTGLDFIPGLHPILTLKMDQTLAV 60

Qy 61 YQQLTSMPSNRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGY 120
 Db 61 YQQLTSMPSNRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGY 120

Qy 121 TEVVALSRLOGLQDMLWQLDLSPGC 146
 Db 121 TEVVALSRLOGLQDMLWQLDLSPGC 146

RESULT 15

AA43311
 ID AA43311 standard; protein; 146 AA.
 XX
 AC AA43311;
 XX
 DT 21-JAN-2000 (first entry)
 XX
 DE Human leptin.
 XX
 KW Leptin; brain function improver; brain denaturation disease; therapy;
 KW Alzheimer's disease; old age dementia; Pick's disease;
 KW hereditary aphasia; Huntington's chorea; Parkinson's disease;
 KW progressive subcutaneous gliosis; progressive supranuclear paralysis;
 KW thalamus denaturation; myoclonus epilepsy.
 XX
 OS Homo sapiens.
 XX
 PN JP11279074-A.
 XX
 PD 12-OCT-1999.
 XX
 PF 26-MAR-1998; 98JP-00100202.
 XX
 PR 26-MAR-1998; 98JP-00100202.
 XX
 PA (OMUR/) OMURA H.
 PA (HORI/) HORI N.
 -PA (SHIR/) SHIRAIISHI T.
 PA (SASA/) SASAKI K.
 PA (TAKE/) TAKEDA H.

PA (TSUJ/) TSUJI M.
 PA (MATS/) MATSUMIYA T.
 XX
 DR WPI; 1999-629222/54.
 XX
 PT A brain function improver - useful for treating brain disorientation
 PT diseases.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC This sequence represents human leptin. The invention relates to a brain
 CC function improver containing mammalian leptin as the active component.
 CC The brain function improver is useful as a treating agent for brain
 CC denaturation diseases such as Alzheimer's disease, old age dementia,
 CC Pick's disease, Huntington's chorea, Parkinson's disease, Parkinson
 CC syndrome, progressive subcutaneous gliosis, progressive supranuclear
 CC paralysis, thalamus denaturation, hereditary aphasia and myoclonus
 CC epilepsy, and other diseases causing deterioration of brain function
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 9e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSQKQVGTGLDFIPGLHPILTLKMDQTLAV 60
 Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSQKQVGTGLDFIPGLHPILTLKMDQTLAV 60

Qy 61 YQQLTSMPSNRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGY 120
 Db 61 YQQLTSMPSNRNVQISNDLENRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGY 120

Qy 121 TEVVALSRLOGLQDMLWQLDLSPGC 146
 Db 121 TEVVALSRLOGLQDMLWQLDLSPGC 146

Search completed: May 4, 2006, 21:52:18
 Job time : 140.474 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: May 4, 2006, 21:50:51 ; Search time 27.5945 seconds
(without alignments)
509.074 Million cell updates/sec
Title: US-10-623-189-1
Perfect score: 736
Sequence: 1 VPIQKVQDDTKTLIKTIVTR.....SRLGSLQDMLWQLDLSPGC 146
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR_80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	167	1 LTHU	leptin precursor -
2	720.5	97.9	166	2 I33166	leptin precursor -
3	619	84.1	167	1 LTMS	leptin precursor -
4	605	82.2	167	1 LTRT	leptin precursor -
5	605	82.2	167	2 I55622	rat ob - rat
6	81.5	11.1	1600	2 A33281	glutamate dehydrog
7	80.5	10.9	444	2 S34039	hypothetical prote
8	79	10.7	829	2 T01362	probable myosin he
9	79	10.7	952	2 H84583	hypothetical prote
10	78	10.6	420	2 S75514	sensory transducti
11	78	10.6	639	2 A10055	probable soluble l
12	77.5	10.5	574	1 B42374	phosphotransferase
13	76.5	10.4	173	2 S77486	ribosomal protein
14	76.5	10.4	362	2 A33967	carbamoyl-phosphat
15	76.5	10.4	822	2 E86305	probable trehalose
16	76	10.3	409	2 B89954	hypothetical prote
17	76	10.3	570	2 T46011	hypothetical prote
18	76	10.3	1036	2 D70117	acri flavine resist
19	75.5	10.3	403	2 T26551	hypothetical prote
20	75.5	10.3	1438	2 S59792	probable membrane
21	75	10.2	142	2 C72430	hypothetical prote
22	75	10.2	296	2 D70424	5,10-methylenetet
23	75	10.2	424	2 E81358	glutamate-1-semial
24	75	10.2	1191	2 S76414	beta transducin-li
25	74.5	10.1	559	2 AB2202	hypothetical prote
26	74.5	10.1	674	2 S46092	probable membrane
27	74	10.1	177	2 A28106	prolactin, 20K - M
28	74	10.1	200	2 B32477	prolactin II precu
29	74	10.1	421	2 AB2959	exopolysaccharide

RESULT 1
LTHU
leptin precursor - human
N;Alternate names: obese protein; obesity factor
C;Species: Homo sapiens (man)
C;Date: 28-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: A38952; JE0148
R;Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A;Title: Positional cloning of the mouse obese gene and its human homologue.
A;Reference number: S50863; MUID:95075453; PMID:7984236
A;Accession: A38952
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-167 <ZHA>
A;Cross-references: UNIPROT:P41159; UNIPARC:UPI00000308D4; GB:U18915; NID:96233331; PID:
R;Liao, H.J.; Deng, Y.B.; Chen, X.M.; Ye, Y.Z.
Chinese Biochem. J. 13, 249-253, 1997
A;Title: Cloning of chinese obesity gene and construction of prokaryotic expression ve
A;Reference number: JE0148
A;Accession: JE0148
A;Molecule type: mRNA
A;Residues: 'M', 22-167 <LIA>
A;Cross-references: UNIPARC:UPI0000158347
A;Experimental source: adipose
A;Note: The author translated GAC for residue 148 as Ser
C;Genetics:
A;Gene: GDB:LEP; OB; OBS
A;Cross-references: GDB:I36420; OMIM:164160
A;Map position: 7q31.3-7q31.3
C;Superfamily: leptin
C;Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>

Query Match	100.0%;	Score 736;	DB 1;	Length 167;
Best Local Similarity	100.0%;	Pred. No. 1.6e-59;		
Matches 146;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	VPIQKVQDDTKTLIKTIVTRINDISHTOSVSKQKVTGLDFTPLGLHPILTSLKMDQTLAV	60	
Db	22	VPIQKVQDDTKTLIKTIVTRINDISHTOSVSKQKVTGLDFTPLGLHPILTSLKMDQTLAV	81	
QY	61	YQOILTSPNSRNVTQISNDLENLRDLHLVLAFLPSKCHLPWASGLTFLDSGLGVLEASGVS	120	
Db	82	YQOILTSPNSRNVTQISNDLENLRDLHLVLAFLPSKCHLPWASGLTFLDSGLGVLEASGVS	141	
QY	121	TEWVALSRQGSLODMLWQLDLSPGC	146	
Db	142	TEWVALSRQGSLODMLWQLDLSPGC	167	

exopolysaccharide
alkaline phosphata
kinesin family pro
probable methyl-ac
hypothetical prote
conserved hypochet
ATP-dependent RNA
type III secretion
hypothetical prote
phenylalanine-TRNA
probable yopC/gen
probable membrane
hypothetical prote
keratin 20, type I
14-nm filament pro
hypothetical prote

RESULT 2
1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
leptin precursor - human
N/Alternate names: obese
C/Species: Homo sapiens (man)
C/Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C/Accession: I53166; G02328
R/Masuzaki, H.; Ogawa, Y.; Isse, N.; Satoh, N.; Okazaki, T.; Shigemoto, M.; Mori, K.; Ta
Diabetes 44, 855-858, 1995
A/Title: Human obese gene expression. Adipocyte-specific expression and regional differ
A/Reference number: I53166; MUID:9530956; PMID:7789654
A/Accession: I53166
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-166 <RES>
A/Cross-references: UNIPROT:P41159; UNIPARC:UPI0000014D164; GB:D49487; NID:g904211; PIDN:
R/Chehab, F.F.; Kim, M.E.
submitted to the EMBL Data Library, December 1995
A/Reference number: H01063
A/Accession: G02328
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-166 <CHE>
A/Cross-references: UNIPARC:UPI000014D164; EMBL:U43415; NID:g1163105; PIDN:AAC31660.1; F
C/Genetics:
A/Gene: GDB:LEP; OB; OBS
A/Cross-references: GDB:136420; OMIM:164160
A/Map position: 7q32.1-7q32.1
A/Introns: 48/3
C/Supfamily: leptin

Query Match 97.9%; Score 720.5; DB 2; Length 166;
Best Local Similarity 99.3%; Pred. No. 4e-58; Indels 1; Gaps 1;
Matches 145; Conservative 0; Mismatches 0

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 80
QY 61 YQIILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSIGGVLEASGYS 120
DB 81 YQIILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSIGGVLEASGYS 140
QY 121 TEVVALSRLOGLQDMLWQDLSPGC 146
DB 141 TEVVALSRLOGLQDMLWQDLSPGC 166

RESULT 3
LTVS
leptin precursor - mouse
N/Alternate names: obese protein
C/Species: Mus musculus (house mouse)
C/Date: 14-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C/Accession: S50863
R/Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A/Title: Positional cloning of the mouse obese gene and its human homologue.
A/Reference number: S50863; MUID:95075453; PMID:7984236
A/Accession: S50863
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-167 <ZHA>
A/Cross-references: UNIPROT:P41160; UNIPARC:UPI0000003FAA; EMBL:U18812; NID:g746416; PID
C/Supfamily: leptin
C/Keywords: adipose tissue
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-167/Product: leptin #status predicted <MAT>

Query Match 84.1%; Score 619; DB 1; Length 167;
Best Local Similarity 84.9%; Pred. No. 6.4e-49;
Matches 124; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKTIVTRINDISHTQSVSAQRVTGLDFIPGLHPILTLKMDQTLAV 81
QY 61 YQIILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSIGGVLEASGYS 120
DB 82 YQIILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSIGGVLEASGYS 141
QY 121 TEVVALSRLOGLQDMLWQDLSPGC 146
DB 142 TEVVALSRLOGLQDMLWQDLSPGC 167

RESULT 4
LTVT
leptin precursor - rat
N/Alternate names: obese protein; obesity factor
C/Species: Rattus norvegicus (Norway rat)
C/Date: 21-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C/Accession: PC4034; JC4142
R/Funahashi, T.; Shimomura, I.; Hiraoka, H.; Arai, T.; Takahashi, M.; Nakamura, T.; Noz
Biochem. Biophys. Res. Commun. 211, 469-475, 1995
A/Title: Enhanced expression of rat obese (ob) gene in adipose tissues of ventromedial
A/Reference number: PC4034; MUID:95314614; PMID:7794258
A/Accession: PC4034
A/Molecule type: mRNA
A/Residues: 1-167 <FUN>
A/Cross-references: UNIPROT:P50596; UNIPARC:UPI0000038DAF
A/Experimental source: adipose tissue
A/Note: The authors translated the codon AAA for residue 32 as Thr
R/Murakami, T.; Shima, K.
Biochem. Biophys. Res. Commun. 209, 944-952, 1995
A/Title: Cloning of rat obese cDNA and its expression in obese rats.
A/Reference number: JC4142; MUID:95251725; PMID:7733988
A/Accession: JC4142
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-167 <MUR>
A/Cross-references: UNIPARC:UPI0000038DAF; DDBJ:D49653; NID:g995614; PIDN:BAA08529.1; P
A/Experimental source: liver
C/Comment: This protein is proposed to function as part of a signalling pathway from ad
C/Genetics:
A/Gene: obese
C/Supfamily: leptin
C/Keywords: adipose tissue
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-167/Product: leptin #status predicted <MAT>

Query Match 82.2%; Score 605; DB 1; Length 167;
Best Local Similarity 83.6%; Pred. No. 1.2e-47;
Matches 122; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKTIVTRINDISHTQSVSAQRVTGLDFIPGLHPILTLKMDQTLAV 81
QY 61 YQIILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSIGGVLEASGYS 120
DB 82 YQIILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSIGGVLEASGYS 141
QY 121 TEVVALSRLOGLQDMLWQDLSPGC 146
DB 142 TEVVALSRLOGLQDMLWQDLSPGC 167

RESULT 5
I55622
rat ob - rat
C/Species: Rattus sp. (rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C/Accession: I55622
R/Ogawa, Y.; Masuzaki, H.; Isse, N.; Okazaki, T.; Mori, K.; Shigemoto, M.; Satoh, N.; T
J. Clin. Invest. 96, 1647-1652, 1995

A>Description: Arabidopsis thaliana chromosome II BAC T29P13 genomic sequence.
A:Reference number: Z14179
A:Accession: T01362
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-829 <ROU>
A:Cross-references: UNIPROT:O64584; UNIPARC:UPI000004A13E; EMBL:AC003096; NID:G3132459

RESULT 12

B42374
phosphotransferase system enzyme I (EC 2.7.3.9) - *Staphylococcus carnosus*
C:Species: *Staphylococcus carnosus*
C>Date: 10-Jul-1992 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C:Accession: B42374; S17075
R:Kohlbrecher, D.; Eisermann, R.; Hengstenberg, W.
J. Bacteriol. 174, 2208-2214, 1992
A:Title: *Staphylococcal* phosphoenolpyruvate-dependent phosphotransferase system: molecular studies of the gene product.
A:Reference number: A42374; MUID:92202148; PMID:1551842
A:Accession: B42374
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-574 <KOH>
A:Cross-references: UNIPROT:P23533; UNIPARC:UPI000013287C; GB:M69050; NID:g153073; PIDN:R:Eisermann, R.; Fischer, R.; Kessler, U.; Neubauer, A.; Hengstenberg, W.
Eur. J. Biochem. 197, 9-14, 1991
A:Title: *Staphylococcal* phosphoenolpyruvate-dependent phosphotransferase system. Purification and cloning of the *ptsH* gene.
A:Reference number: S15367; MUID:91200066; PMID:1901791
A:Accession: S17075
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <EIS>
A:Cross-references: UNIPARC:UPI000017007F; EMBL:X60766; NID:g46907; PIDN:CAA43176.1; PIDC:Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I homologous domain: phosphotransferase system enzyme I; phosphotransferase; sugar transport system F;5-563/Domain: phosphotransferase system enzyme I homology <PT1>

Query Match 10.5%; Score 77.5; DB 1; Length 574;
Best Local Similarity 25.0%; Pred. No. 34;
Matches 32; Conservative 27; Mismatches 54; Indels 15; Gaps 5;
Qy 11 KTLIKTIVTR---INDISHTQSVSKQKVTGLDFIPGLHPLTLTKSKMDQTLAVYQOILTS 67
Db 188 RTSHSAIMSRLSLEIPAVVGTGKSTEEVEAGDTIVVDGTMGDLINPDSDEVIAYQE---- 243
Qy 68 MPSRNVQISNDLENLRLHLVAFSKCHLPWASGLETLDLSGLGVLE---ASG---YSTE 122
Db 244 -KRENFNFKQKQKLDKDAESVTA--DGHVVELAANIQTNDLPGLVIENGAEGIGLYRTE 300
Qy 123 VVALSRQLQ 130
Db 301 FLYMGDRQ 308

RESULT 13

S77486
ribosomal protein S5 - *Synechocystis* sp. (strain PCC 6803)
N:Alternate names: protein sll1812
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S77486
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S77486
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173 <KAN>
A:Cross-references: UNIPROT:P73304; UNIPARC:UPI000013507A; EMBL:D90905; GB:AB001339; NID:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: rps5
A:Superfamily: ribosomal protein S5/S2
C:Keywords: protein biosynthesis; ribosome

Query Match 10.4%; Score 76.5; DB 2; Length 173;
Best Local Similarity 31.2%; Pred. No. 9.2;
Matches 29; Conservative 12; Mismatches 41; Indels 11; Gaps 3;
Qy 6 VQDDTKTIKTIIVTRINDISH-TQSVSSKQKVTGLDFIPG-----LHPILTLTKMDQ 56
Db 70 VADKKQLIIEVPLTKNSIHTINGVSGAKVVRPAAPGTGVTAGAVRTVLELAGVKN 129
Qy 57 TLAVYQOILTSMPSPNRNVQISNDLENLRLHLV 89
Db 130 ILA--KQLGSNNPLNARAAINALETLTPTSEV 160

RESULT 14

A83967
carbamoyl-phosphate synthetase (glutaminase subunit) pyzAA [imported] - *Bacillus halodurans*
C:Species: *Bacillus halodurans*
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: A83967
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, P.; Hir Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and sequencing of the *ptsH* gene.
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: A83967
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <STO>
A:Cross-references: UNIPROT:Q9K9V8; UNIPARC:UPI0000126F32; GB:AP001515; GB:BA000004; NID:Experimental source: strain C-125
C:Genetics:
A:Gene: pyzAA
C:Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbam

Query Match 10.4%; Score 76.5; DB 2; Length 362;
Best Local Similarity 31.0%; Pred. No. 23;
Matches 22; Conservative 15; Mismatches 27; Indels 7; Gaps 3;
Qy 78 NDLENRLDLHLVAFSKCHLP--WASGLETLDLSGLGVLEASGYG----TEVVALSRLOQ 131
Db 66 DDPESMPNPAIHGLIVKEACDIPSNRSE-ESLDSLKAKQIPGLSGIDTRKLTRLRMHG 124
Qy 132 SLQDMLWQLDL 142
Db 125 TLKQQLCPLDV 135

RESULT 15

E86305
probable trehalose-6-phosphate synthase [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86305
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federapfel, M.A.; Kaul, S.; White, O.; Alonah Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasey, T.H.; Dewar, K. Nature 408, 815-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86305
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-822 <STO>
A:Cross-references: UNIPROT:Q9FZ57; UNIPARC:UPI00000A0CF7; GB:AE005172; NID:g9802765; C:Genetics:
A:Map position: 1

Query Match 10.4%; Score 76.5; DB 2; Length 822;
Best Local Similarity 31.6%; Pred. No. 66;

Matches 31; Conservative 16; Mismatches 36; Indels 15; Gaps 4;
-Qy 38 GLDFIPGLHPIILTSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRDLLHVLAFKSCH 97
Db 470 GLDFMSELNGIIPESQM-----RKIPLOPEQDVIIQQYSQSN---RLIILGFFGTLA 521
Qy 98 LPWASGLETLD-----SLGGVLEA--SGYSTEVVALSR 128
Db 522 EPMNSGTKEMDLKLNPELKGTLKALCNDPKTTVVVLSR 559

Search completed: May 4, 2006, 22:03:30
Job time : 28.5945 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:47:48 ; Search time 145.498 Seconds
(without alignments)
707.961 Million cell updates/sec

Title: US-10-623-189-1
Perfect score: 736
Sequence: 1 VPIQVQDDTKTLIKTIVTR.....SRLQSSIQDMLQDLSPGC 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	736	100.0	167	1	OB_HUMAN	P41159 homo sapien
2	736	100.0	167	1	OB_HUMAN	O6nt58 homo sapien
3	733	99.6	146	1	OB_PANTR	O02750 pan troglod
4	728	98.9	146	1	OB_GORGO	Q95189 gorilla gor
5	721	98.0	146	1	OB_PONPY	Q95234 pongo pygma
6	672	91.3	167	1	OB_MACMU	Q28504 macaca mula
7	639	86.8	167	1	OB_FELCA	Q9n2c1 felis silve
8	628	85.3	146	2	O6T8R8 RUBBU	O6T8R8 bubalus bub
9	628	85.3	167	1	OB_BOVIN	P50595 bos taurus
10	628	85.3	167	1	OB_RUBBU	Q5J732 bubalus bub
11	627	85.2	167	1	OB_PIG	Q29406 sus scrofa
12	627	85.2	167	2	Q5TIL9 PTG	Q5TIL9 sus scrofa
13	624	84.8	146	1	OB_SHEEP	Q28603 ovis aries
14	624	84.8	167	1	O5EAE4 BOVIN	O5EAE4 bos taurus
15	619	84.1	146	2	Q4VW71 CTEID	Q4VW71 ctenopharyn
16	619	84.1	167	1	OB_MOUSE	P41160 mus musculus
17	619	84.1	167	2	Q544U0 MOUSE	Q544U0 mus musculus
18	615	83.6	146	2	Q4VW70 HYPMO	Q4VW70 hypophthalm
19	615	83.6	146	2	Q4VW72 CARAU	Q4VW72 carassius a
20	615	83.6	146	2	Q41LM8 CYPECA	Q41LM8 cyprinus ca
21	612	83.2	146	2	Q4VW67 MEGAM	Q4VW67 megalobrama
22	609	82.7	146	2	Q4VW68 SILAS	Q4VW68 silurus aso
23	605	82.2	167	1	OB_RAT	P50596 rattus norv
24	604	82.1	146	2	Q4VW66 9PERC	Q4VW66 channa argu
25	604	82.1	146	2	Q4VW81 9TELE	Q4VW81 culter sp.
26	603.5	82.0	147	2	Q4VW60 ANAPL	Q4VW60 anas platyr
27	597	81.1	146	2	Q4VW69 ARINO	Q4VW69 aristichthy
28	596	81.0	167	1	OB_CANFA	O02720 canis fami
29	586.5	79.7	163	1	OB_CHICK	O42164 gallus gall
30	576.5	78.3	145	1	OB_MELGA	O93416 meleagris g
31	522.5	71.0	145	1	OB_HORSE	O9tu09 equus cabal

32 505 68.6 167 1 OB_SMICR
33 499 67.8 118 2 Q4VYB6_9RODE
34 498 67.7 119 2 Q861R2_BUBBU
35 477 64.8 118 2 Q8MK60_ALOLA
36 476 64.7 118 2 Q8MK58_VULVU
37 474 64.4 118 2 Q8MK59_NYCPR
38 469 63.7 118 2 Q8MK61_CANFA
39 465 63.2 167 1 OB_HALGR
40 463 62.9 167 1 OB_PROVI
41 462 62.8 123 2 Q95KW9_MYOIU
42 457 62.1 110 2 Q56QP8_SHEEP
43 449 61.0 109 2 Q866S7_BUBBU
44 439 59.6 109 2 Q864V1_CAMDR
45 387 52.6 106 2 Q95WGS_CAPHI

ALIGNMENTS

RESULT 1
OB_HUMAN STANDARD; PRT; 167 AA.
AC P41159; O15158; Q56A88;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Leptin precursor (Obesity factor) (Obese protein).
GN Name=LEP; Synonyms=OB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95015453; PubMed=7984236; DOI=10.1038/372425a0;
RX Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RT "Positional cloning of the mouse obese gene and its human homologue."
RL Nature 372:425-432(1994).
RN [2]
RP ERATUM.
RA Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RL Nature 374:479-479(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95309556; PubMed=7789654;
RX Masuzaki H., Ogawa Y., Isse N., Satoh N., Okazaki T., Shigemoto M.,
RA Mori K., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,
RA Nakao K.;
RT "Human obese gene expression. Adipocyte-specific expression and
regional differences in the adipose tissue."
RL Diabetes 44:855-858(1995).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96223958; PubMed=8626726; DOI=10.1074/jbc.271.8.3971;
RX Gong D.W., Bi S., Pratley R.E., Weintraub B.D.;
RT "Genomic structure and promoter analysis of the human obese gene."
RL J. Biol. Chem. 271:3971-3974(1996).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Chehab F.P., Lim M.E.;
RA Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96070903; PubMed=7499240; DOI=10.1074/jbc.270.46.27728;
RX Isse N., Ogawa Y., Tamura N., Masuzaki H., Mori K., Okazaki T.,
RA Satoh N., Shigemoto M., Yoshimasa Y., Nishi S., Hosada K., Inazawa J.,
RA Nakao K.;
RT "Structural organization and chromosomal assignment of the human obese
gene."
RL J. Biol. Chem. 270:27728-27733(1995).
RN [7]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=96198511; PubMed=8621021;
 RA Niki T., Mori H., Tamori Y., Kishimoto-Hashiramoto M., Ueno H.,
 RA Araki S., Masugi J., Sawant N., Majithia H.R., Rais N.,
 RA Hashiramoto M., Taniguchi H., Kasuga M.;
 RT "Human obese gene: molecular screening in Japanese and Asian Indian
 RT NIDDM patients associated with obesity.";
 RL Diabetes 45:675-678(1996).
 [8]
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RA Lu L., Fu Z., Xu M., Fu Y., Hu Z.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 [9]
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT MET-94.
 RA Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Bartucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
 RT "SeattleSNPs: NHLBI H66682 program for genomic applications, UW-
 RT FRCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 [10]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Placenta; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.C., Trichman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Glimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [11]
 RN INTERACTION WITH SIGLEC6.
 RX MEDLINE=99357812; PubMed=10428856; DOI=10.1074/jbc.274.32.22729;
 RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
 RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
 RA Varki A., Kastelein R.A.;
 RT "OB-BP1/Siglec-6. A leptin- and sialic acid-binding protein of the
 RT immunoglobulin superfamily.";
 RL J. Biol. Chem. 274:22729-22738(1999).
 [12]
 RN ERRATUM.
 RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
 RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
 RA Varki A., Kastelein R.A.;
 RL J. Biol. Chem. 274:28058-28058(1999).
 [13]
 RN STRUCTURE BY NMR.
 RP MEDLINE=97309492; PubMed=9166907; DOI=10.1016/S0014-5793(97)00353-0;
 RA Kline A.D., Becker G.W., Churgay L.M., Landen B.E., Martin D.K.,
 RA Muth W.L., Rathnachalam R., Richardson J.M., Schoner B., Ulmer M.,
 RA Hale J.E.;
 RT "Leptin is a four-helix bundle: secondary structure by NMR.";
 RL FEBS Lett. 407:239-242(1997).
 [14]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=97289390; PubMed=9144295;
 RA Zhang F., Basinski M.B., Beals J.M., Briggs S.L., Churgay L.M.,
 RA Clawson D.K., Dimarchi R.D., Furman T.C., Hale J.E., Hsiung H.M.,
 RA Schoner B.E., Smith D.P., Zhang X.Y., Wery J.P., Schevitz R.W.;
 RT "Crystal structure of the obese protein leptin-E100.";
 RL Nature 387:206-209(1997).

RN VARIANT MET-94.
 RA Bartholomew D.W., McClellan J.M.;
 RT "A novel polymorphism in the leptin gene.";
 RL Hum. Mutat. 12:220-220(1998).
 [16]
 RN VARIANT MORBID OBESITY TRP-105.
 RX MEDLINE=98160176; PubMed=9500540;
 RA Strobel A., Issad T., Camoin L., Ozata M., Stroberg A.D.;
 RT "A leptin missense mutation associated with hypogonadism and morbid
 RT obesity.";
 RL Nat. Genet. 18:213-215(1998).
 CC -1- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass.
 CC -1- SUBUNIT: Interacts with SIGLEC6.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: Defects in LEP may be a cause of autosomal recessive
 CC obesity [MIM:601665].
 CC -1- SIMILARITY: Belongs to the leptin family.
 CC -1- DATABASE: NAME=RD Systems' cytokine mini-reviews: LEP;
 CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=213".

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 DR EMBL; U18915; AAA60470.1; -; mRNA.
 DR EMBL; D49487; BAA08448.1; -; mRNA.
 DR EMBL; U43653; AAC50400.1; -; mRNA.
 DR EMBL; U43415; AAC31660.1; -; Genomic DNA.
 DR EMBL; D63710; BAA09839.1; -; Genomic DNA.
 DR EMBL; D63519; BAA09787.1; -; Genomic DNA.
 DR EMBL; AF008123; AAB63507.1; -; mRNA.
 DR EMBL; AY96373; AAB81413.1; -; Genomic DNA.
 DR EMBL; BC060830; AAB60830.1; -; mRNA.
 DR EMBL; BC069452; AAB69452.1; -; mRNA.
 DR EMBL; BC069527; AAB69527.1; -; mRNA.
 DR PIR; A38952; LTHU.
 DR PIR; I53166; I53166.
 DR PDB; 1AX8; X-ray; @=22-167.
 DR Ensembl; ENSG00000174697; Homo sapiens.
 DR HGNC; HGNC:6553; LEP.
 DR MIM; 164160; -.
 DR MIM; 601665; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0006112; P:energy reserve metabolism; TAS.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR PANTHER; PTHR11724; Leptin; 1.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 DR 3D-structure; Diabetes mellitus; Disease mutation; Obesity;
 DR Polymorphism; Signal.
 KW SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167
 FT VARIANT 49 49 Missing (in 30% the clones).
 FT VARIANT 94 94 /FTID=VAR_004196.
 FT VARIANT 105 105 V -> M (in dbSNP:17151919).
 FT VARIANT 110 110 R -> W (in morbid obesity and
 FT hypogonadism).
 FT VARIANT 110 110 /FTID=VAR_008094.
 FT VARIANT 96 96 V -> M (in dbSNP:1800564).
 FT CONFLICT 96 96 /FTID=VAR_011955.
 FT HELIX 25 44 Q -> R (in Ref. 8).

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FT HELIX 72 87
FT TURN 88 88

Query Match 100.0%; Score 736; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.1e-60; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
DB 22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 81

QY 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
DB 82 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 141

QY 121 TEVVALSRQSGSLQDMLWQDLSPGC 146
DB 142 TEVVALSRQSGSLQDMLWQDLSPGC 167

RESULT 2
Q6NT58_HUMAN
ID Q6NT58_HUMAN PRELIMINARY; PRT; 167 AA.
AC Q6NT58;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Leptin.
GN Name=LEP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426030999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC EMBL; BC069323; AA069323.1; -; mRNA.
CC DR HSSP; P41159; IAX8.
CC SMR; Q6NT58; 24-167.
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DR Ensembl; ENSG00000174697; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR000085; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
SQ SEQUENCE 167 AA; 18613 MW; BE1A046PFB1554DE CRC64;

Query Match 100.0%; Score 736; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.1e-60; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
DB 22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 81

QY 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
DB 82 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 141

QY 121 TEVVALSRQSGSLQDMLWQDLSPGC 146
DB 142 TEVVALSRQSGSLQDMLWQDLSPGC 167

RESULT 3
OB_PANTR
ID OB_PANTR STANDARD; PRT; 146 AA.
AC O02750;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
RC Rockey P.K., Rostock P.R.;
RA "Cloning of obese genes from different species: a comparison of the
gene structures and the sequences of the obese gene products,
leptin."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL; U96450; AA054023.1; -; mRNA.
CC DR HSSP; P41159; IAX8.
CC SMR; O02750; 3-146.
CC InterPro; IPR012351; Cytokine_4_hlx.
CC InterPro; IPR000065; Leptin.
CC PANTHER; PTHR11724; Leptin; 1.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
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Db 61 YQOILTSMPNRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTDLRLGGVLEASGYS 120
QY 121 TEVVALSRQSGSLQDMLWQLDLSGPC 146
Db 121 TEVVALSRQSGSLQDMLWQLDLSGPC 146

RESULT 6
OB_MACWU
ID_ OB_MACWU STANDARD; PRT; 167 AA.
AC Q28504;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OC Felidae; Felis.
OC NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adipose tissue;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Nicolson M.A.,
RA Hansen B.C.;
RT "Regulation of obese (ob) mRNA and plasma leptin levels in rhesus
RT monkeys. Effects of insulin, body weight, and non-insulin-dependent
RT diabetes mellitus."
RT J. Biol. Chem. 271:25327-25331(1996).
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U58492; AAC50730.1; -; mRNA.
CC HSP; P41159; IAX8.
CC SMR; Q28504; 24-167.
CC InterPro; IPR012351; Cytokine_4_hlx.
CC DR PANTHER; PTHR11724; Leptin; 1.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC KW Obesity; Signal.
CC SIGNAL 1 21 Potential.
CC CHAIN 22 167 Leptin.
CC DISULFID 117 167 By similarity.
CC SEQUENCE 167 AA; 18953 MW; E7D9F30628A5BBE9 CRC64;

Query Match
Best Local Similarity 91.3%; Score 672; DB 1; Length 167;
Matches 133; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 VPIQKVDQDTKTLIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLSKMDQTLAV 60
Db 22 VPIQKVDQDTKTLIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLSKMDQTLAI 81

QY 61 YQOILTSMPNRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTDLRLGGVLEASGYS 120
Db 82 YQOILNLPNRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTDLRLGGVLEASLYS 141

QY 121 TEVVALSRQSGSLQDMLWQLDLSGPC 146

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Db 142 TEVVALSRQSGSLQDMLWQLDLSGPC 167

RESULT 7
OB_FELCA
ID_ OB_FELCA STANDARD; PRT; 167 AA.
AC Q9N2C1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OC NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=White adipose tissue;
RA Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;
RT "Molecular cloning of feline leptin cDNA."
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AB041360; BAA95481.1; -; mRNA.
CC HSP; P41159; IAX8.
CC SMR; Q9N2C1; 24-167.
CC InterPro; IPR012351; Cytokine_4_hlx.
CC DR InterPro; IPR000065; Leptin.
CC DR PANTHER; PTHR11724; Leptin; 1.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC KW Obesity; Signal.
CC SIGNAL 1 21 Potential.
CC CHAIN 22 167 Leptin.
CC DISULFID 117 167 By similarity.
CC SEQUENCE 167 AA; 18584 MW; 643720DBB0A84B95 CRC64;

Query Match
Best Local Similarity 86.8%; Score 639; DB 1; Length 167;
Matches 126; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIQKVDQDTKTLIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLSKMDQTLAV 60
Db 22 VPIQKVDQDTKTLIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLSKMDQTLAI 81

QY 61 YQOILTSMPNRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTDLRLGGVLEASGYS 120
Db 82 YQOILTGLPNRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTDLRLGGVLEASLYS 141

QY 121 TEVVALSRQSGSLQDMLWQLDLSGPC 146
Db 142 TEVVALSRQSGSLQDMLWQLDLSGPC 167

RESULT 8
Q6T8R8_BUBBU

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ID QGTR88 BUBBU PRELIMINARY; PRT; 146 AA.
AC QGTR88;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Leptin (Fragment).
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=adipose tissue;
RA Rajendran S., Shukla D.C., Saravanan B.C.;
RT "Cloning and sequencing of buffalo leptin gene.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY427959; AAR05862.1; -; mRNA.
DR HSSP; P41159; IAX8.
DR SMR; Q678R8; 3-146.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1. leptin.
FT CHAIN <1 146
FT NON_TER 1
SQ SEQUENCE 146 AA; 16069 MW; 1A745EE0851BD8CA CRC64;

Query Match 85.3%; Score 628; DB 2; Length 146;
Best Local Similarity 87.0%; Pred. No. 7.1e-50;
Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIKQVQDDTKLIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VPRIKQVQDDTKLIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAI 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 YQILTSMPERNVIQISNDLENRLDLHLVAFKSKCHLPWASGLETLDSGGVLEASGYS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YQILTSMPERNVIQISNDLENRLDLHLVAFKSKCHLPWASGLETLDSGGVLEASLSYS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 TEVVALSRLOGLQDMLWLDLSPGC 146
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TEVVALSRLOGLQDMLRQLDLSPGC 146
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
OB_BOVIN STANDARD; PRT; 167 AA.
AC P50595; O97918; Q95133; Q9TS29;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Names=LEP; Synonyms=OB, OBS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Tellam R.L., Briscoe S., Vuocolo A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE OF 22-167.
RA Ji S., Spurlock M.E.;
RT "Partial cloning of bovine obesity gene.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 22-167.
RC TISSUE=White adipose tissue;
RA Kawakita Y., Abe H., Miyashige T.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS CYS-25 AND VAL-80.
RC STRAIN=Jersey;
RX MEDLINE=20063685; PubMed=10594237; DOI=10.1007/s003359901180;
RA Konfortov B.A., Licence V.E., Miller J.R.;
RT "Resequencing of DNA from a diverse panel of cattle reveals a high
level of polymorphism in both intron and exon.";
RL Mamm. Genome 10:1142-1145(1999).
RN [5]
RP NUCLEOTIDE SEQUENCE, AND VARIANT CYS-25.
RA Liefers S.C.;
RT "Genotype effects of bovine leptin mutations on pre- and postpartum
leptin concentrations.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE OF 46-145.
RA Lien S., Sundvold H., Klungland H., Vaage D.I.;
RT "Two novel polymorphisms in the bovine obesity gene (OBS).";
RL Anim. Genet. 28:245-245(1997).
RN [7]
RP NUCLEOTIDE SEQUENCE OF 60-146.
RX MEDLINE=96269621; PubMed=8661738; DOI=10.1007/s003359900118;
RA Pfister-Genskow M.A., Hayes H., Eggen A., Bishop M.D.;
RT "Chromosomal localization of the bovine obesity (OBS) gene.";
RL Mamm. Genome 7:398-399(1996).
RN [8]
RP NUCLEOTIDE SEQUENCE OF 1-48.
RA Fitzsimmons C.J., Schmutz S.M.;
RT "Exon two of the bovine obese, leptin, gene.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; U43943; AAA85906.1; -; mRNA.
DR EMBL; U50365; AAB61244.1; -; Genomic_DNA.
DR EMBL; U65793; AAB06579.1; -; mRNA.
DR EMBL; AB003143; BAA19750.1; -; mRNA.
DR EMBL; AJ132764; CAB64255.1; -; Genomic DNA.
DR EMBL; AJ236854; CAB38018.1; -; Genomic DNA.
DR EMBL; AJ512638; CAD54745.1; -; Genomic DNA.
DR EMBL; AJ512639; CAD54745.1; JOINED; Genomic_DNA.
DR EMBL; Y11369; CAA72197.1; -; Genomic_DNA.
DR EMBL; U43833; AAB18762.1; -; Genomic_DNA.
DR EMBL; AF10500; AAD23567.1; -; Genomic_DNA.
DR HSSP; P41159; IAX8.
DR SMR; P50595; 24-167.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR000065; Leptin.
DR PANTHER; PTHR11724; Leptin; 1.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity; Polymorphism; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT VARIANT 25 25 R -> C.
FT VARIANT 80 80 A -> V.

```

FT CONFLICT 25 25 R -> Q (in Ref. 2).
 FT CONFLICT 166 166 G -> E (in Ref. 2).
 SQ SEQUENCE 167 AA; 18716 MW; 94C666B3069E50B7 CRC64;

Query Match 85.3%; Score 628; DB 1; Length 167;
 Best Local Similarity 87.0%; Pred. No. 8.3e-50;
 Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VPIKQVDDTKTLIKTIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLISKMDQTLAV 60
 Db 22 VPIKQVDDTKTLIKTIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLISKMDQTLAI 81
 Qy 61 YQILTSMPNRNVQISNDLENLRLDHLVAFSKCHLPWASGLTLDLSLGGVLEASGY 120
 Db 82 YQILTSMPNRNVQISNDLENLRLDHLVAFSKCHLPWASGLTLDLSLGGVLEASGY 141
 Qy 121 TEVALSRLOGLQDMLWQDLSPGC 146
 Db 142 TEVALSRLOGLQDMLRQLDLSFGC 167

RESULT 10
 OB_BUBBU
 ID OB_BUBBU STANDARD; PRT; 167 AA.
 AC Q5J732;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=LEP; Synonyms=OB;
 OS Bubalus bubalis (Domestic water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bubalus.
 OX NCBI_TaxID=89462;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA PubMed=15566470; DOI=10.1111/j.1365-2052.2004.01186.x;
 RX Vallinoto M., Schneider M.P., Silva A., Iannuzzi L., Brenig B.;
 RT "Molecular cloning and analysis of the swamp and river buffalo leptin gene.";
 RL Anim. Genet. 35:462-463 (2004).
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- SIMILARITY: Belongs to the leptin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 DR EMBL; AY495587; AAC86311.1; -; Genomic DNA.
 DR SMR; Q5J732; 24-167.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000065; Leptin.
 DR PANTHER; PTHR11724; Leptin; 1.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 - KW Obesity; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 SQ SEQUENCE 167 AA; 18688 MW; 8524749CB69CAD99 CRC64;

Query Match 85.3%; Score 628; DB 1; Length 167;
 Best Local Similarity 87.0%; Pred. No. 8.3e-50;

Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VPIKQVDDTKTLIKTIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLISKMDQTLAV 60
 Db 22 VPIKQVDDTKTLIKTIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLISKMDQTLAI 81
 Qy 61 YQILTSMPNRNVQISNDLENLRLDHLVAFSKCHLPWASGLTLDLSLGGVLEASGY 120
 Db 82 YQILTSMPNRNVQISNDLENLRLDHLVAFSKCHLPWASGLTLDLSLGGVLEASGY 141
 Qy 121 TEVALSRLOGLQDMLWQDLSPGC 146
 Db 142 TEVALSRLOGLQDMLRQLDLSFGC 167

RESULT 11
 OB_PIG
 ID OB_PIG STANDARD; PRT; 167 AA.
 AC Q29406; O19095; Q95251;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=LEP; Synonyms=OB, OBS;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA TISSUE=Adipose tissue;
 RA Louis C.F.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Ramsay T.G., Yan X.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=Landrace;
 RA Robert C., Palin M.-F., Coulombe N., Roberge C., Silversides P.G.,
 RA Benkel B.F., McKay R.M., Pelletier G.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Bidwell C.A., Ji S., Spurlock M.E.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=Meishan;
 RC Dai R., Li N., Hu X., Wu C.;
 RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RA McNeel R.L., Mersmann H.J.;
 RT "Adipose tissue regulatory transcript expression in lean versus obese pigs".
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Large white;
 RA Soares M.A.M., Euclydes R.F., Guimaraes S.E.F., Martins M.F.,
 RA Lopes P.S.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP NUCLEOTIDE SEQUENCE OF 15-110.
 RC TISSUE=White adipose tissue;
 RX MEDLINE=97009821; PubMed=8856925;
 RA Neuenchwander S., Rettenberger G., Meijerink E., Jorg H.,
 RA Stranzinger G.;
 RT "Partial characterization of porcine obesity gene (OBS) and its localization to chromosome 18 by somatic cell hybrids.";

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 DR EMBL; U84247; AAB41786.1; -; mRNA.
 DR EMBL; U62123; AAB51033.1; -; mRNA.
 DR HSP; P41159; IAX8.
 DR SMR; Q28603; 3-146.
 DR InterPro; IPR012351; Cytochrome 4_hlx.
 DR PANTHER; PTHR11724; Leptin; 1.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 KW Obesity.
 FT DISULFID 96 146 By similarity.
 FT CONFLICT 65 65 L -> H (in Ref. 2).
 FT CONFLICT 92 92 A -> G (in Ref. 2).
 FT CONFLICT 124 124 V -> L (in Ref. 2).
 SQ SEQUENCE 146 AA; 16054 MW; 19D54C53240968CA CRC64;

Query Match 84.8%; Score 624; DB 1; Length 146;
 Best Local Similarity 87.0%; Pred. No. 1.6e-49;
 Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPLTSLSKMDQTLAV 60
 Db 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPLTSLSKMDQTLAI 60
 Qy 61 YQILTSMPSPNRVQISNDLENLDLHLVAFSKCHLPWASGLTLDLSLGGVLEASGYS 120
 Db 61 YQILTSMPSPNRVQISNDLENLDLHLVAFSKCHLPWASGLTLDLSLGGVLEASGYS 120
 Qy 121 TEVALSRQSGSLQDMLWQLDLSGPC 146
 Db 121 TEVALSRQSGSLQDMLWQLDLSGPC 146

RESULT 14

QSEAE4_BOVIN PRELIMINARY; PRT; 167 AA.
 AC QSEAE4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Leptin.
 GN Name=LEP;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pooled;
 RA Smith T.P.L., Grosse W.M., Fraking B.A., Roberts A.J., Stone R.T.,
 RA Casas E., Wray J.E., White J., Cho J., Fahrénkrug S.C., Bennett G.L.,
 RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
 RA Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
 RA Keele J.W.;
 FT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
 RT libraries and construction of a gene index for cattle.";
 RL Genome Res. 11:626-630(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pooled;
 RA Hathay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W.,
 RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
 RT "Sequencing and analysis of Bos taurus full-length insert cDNA
 clones.";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BT020625; AAX08642.1; -; mRNA.

DR SMR; QSEAE4; 24-167.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000065; Leptin.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 SQ SEQUENCE 167 AA; 18663 MW; C9AA16B31AF229CE CRC64;

Query Match 84.8%; Score 624; DB 2; Length 167;
 Best Local Similarity 87.0%; Pred. No. 1.9e-49;
 Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPLTSLSKMDQTLAV 60
 Db 22 VPICKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPLTSLSKMDQTLAI 81
 Qy 61 YQILTSMPSPNRVQISNDLENLDLHLVAFSKCHLPWASGLTLDLSLGGVLEASGYS 120
 Db 82 YQILTSMPSPNRVQISNDLENLDLHLVAFSKCHLPWASGLTLDLSLGGVLEASGYS 141
 Qy 121 TEVALSRQSGSLQDMLWQLDLSGPC 146
 Db 142 TEVALSRQSGSLQDMLWQLDLSGPC 167

RESULT 15

QAVW71_CTEID PRELIMINARY; PRT; 146 AA.
 AC QAVW71;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Obese protein (Fragment).
 OS Ctenopharyngodon idella (Grass carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OC Cyprinidae; Ctenopharyngodon.
 OC NCBI_TaxID=7959;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mesenteric adipose tissue;
 RA Dai H., Long L.;
 RT "Molecular cloning and sequence analysis of the obese gene from the
 RL Ctenopharyngodon idellus.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY551335; AAT45394.1; -; mRNA.
 FT NON_TER 1
 SQ SEQUENCE 146 AA; 16004 MW; 60D1A3BF6EB062AB CRC64;

Query Match 84.1%; Score 619; DB 2; Length 146;
 Best Local Similarity 84.9%; Pred. No. 4.8e-49;
 Matches 124; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPLTSLSKMDQTLAV 60
 Db 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPLTSLSKMDQTLAV 60
 Qy 61 YQILTSMPSPNRVQISNDLENLDLHLVAFSKCHLPWASGLTLDLSLGGVLEASGYS 120
 Db 61 YQVLTSLPSQNVQISNDLENLDLHLVAFSKCHLPWASGLTLDLSLGGVLEASGYS 120
 Qy 121 TEVALSRQSGSLQDMLWQLDLSGPC 146
 Db 121 TEVALSRQSGSLQDMLWQLDLSGPC 146

Search completed: May 4, 2006, 21:57:13
 Job time : 146.498 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:52:45 ; Search time 33.1134 Seconds
(without alignments)
364.525 Million cell updates/sec

Title: US-10-623-189-1
Perfect score: 736
Sequence: 1 VPQKQDDTKTKTIKTIVTR.....SRQGSIQDMLWLQDLSPGC 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCrUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	146	1	US-08-398-021-3 Sequence 3, Appli
2	736	100.0	146	1	US-08-788-943A-5 Sequence 5, Appli
3	736	100.0	146	1	US-08-823-104-3 Sequence 3, Appli
4	736	100.0	146	1	US-09-003-081-6 Sequence 6, Appli
5	736	100.0	146	2	US-08-648-262-6 Sequence 6, Appli
6	736	100.0	146	2	US-08-648-263-6 Sequence 32, Appli
7	736	100.0	146	2	US-09-172-644-1 Sequence 1, Appli
8	736	100.0	146	2	US-09-221-178-1 Sequence 1, Appli
9	736	100.0	146	2	US-09-200-919-1 Sequence 2, Appli
10	736	100.0	146	4	PCT-US96-00952-2 Sequence 2, Appli
11	736	100.0	146	4	PCT-US96-00952-3 Sequence 3, Appli
12	736	100.0	147	2	US-09-200-919-4 Sequence 4, Appli
13	736	100.0	147	2	US-08-429-362-3 Sequence 3, Appli
14	736	100.0	148	1	US-08-823-104-18 Sequence 18, Appli
15	736	100.0	148	1	US-08-540-242A-4 Sequence 4, Appli
16	736	100.0	167	1	US-08-347-563A-4 Sequence 4, Appli
17	736	100.0	167	1	US-09-003-081-5 Sequence 5, Appli
18	736	100.0	167	2	US-08-292-345B-6 Sequence 4, Appli
19	736	100.0	167	2	US-08-648-262-5 Sequence 5, Appli
20	736	100.0	167	2	US-08-648-263-5 Sequence 5, Appli
21	736	100.0	167	2	US-08-488-214A-4 Sequence 4, Appli
22	736	100.0	167	2	US-08-488-214A-4 Sequence 4, Appli
23	736	100.0	167	2	US-08-488-208A-4 Sequence 4, Appli
24	736	100.0	167	2	US-08-759-628-1 Sequence 1, Appli
25	736	100.0	167	2	US-08-688-908-7 Sequence 7, Appli
26	736	100.0	167	2	US-08-483-211A-4 Sequence 4, Appli
27	736	100.0	167	2	US-08-483-211A-4 Sequence 4, Appli

28	736	100.0	167	2	US-08-488-223A-4 Sequence 4, Appli
29	736	100.0	167	2	US-09-147-805-4 Sequence 4, Appli
30	736	100.0	167	2	US-08-438-431A-4 Sequence 4, Appli
31	736	100.0	167	2	US-08-488-225A-4 Sequence 4, Appli
32	736	100.0	167	2	US-09-204-730B-4 Sequence 4, Appli
33	736	100.0	167	2	US-09-316-393-4 Sequence 4, Appli
34	736	100.0	167	2	US-09-377-081-17 Sequence 17, Appli
35	736	100.0	167	2	US-09-686-647A-4 Sequence 4, Appli
36	736	100.0	167	4	PCT-US96-01471-4 Sequence 4, Appli
37	736	100.0	374	2	US-10-679-999-15 Sequence 15, Appli
38	736	100.0	374	2	US-10-679-999-18 Sequence 18, Appli
39	736	100.0	379	2	US-10-679-999-9 Sequence 9, Appli
40	736	100.0	379	2	US-10-679-999-12 Sequence 12, Appli
41	736	100.0	397	2	US-08-775-066-2 Sequence 2, Appli
42	733	99.6	146	2	US-08-914-375C-34 Sequence 34, Appli
43	731	99.3	146	1	US-08-788-943A-2 Sequence 2, Appli
44	731	99.3	146	1	US-08-788-943A-3 Sequence 3, Appli
45	731	99.3	146	1	US-08-823-104-11 Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-08-398-021-3
; Sequence 3, Application US/08398021
; Patent No. 5594101
; GENERAL INFORMATION:
; APPLICANT: Becker, Gerald W.
; APPLICANT: Hale, John E.
; APPLICANT: MacKellar 1, Warren C.
; TITLE OF INVENTION: ANTI-OBESITY PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,021
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P.
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-0757
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-398-021-3

Query Match 100.0%; Score 736; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKQDDTKTKTIKTIVTRINDISHTOSVSSKQKVTGLDFIPGLHPITLTSKMDQTLAV 60
DB 1 VPQKQDDTKTKTIKTIVTRINDISHTOSVSSKQKVTGLDFIPGLHPITLTSKMDQTLAV 60

QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
|
Db 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
QY 121 TEVVLSRLQGSQDMLWQLDLSFGC 146
|
Db 121 TEVVLSRLQGSQDMLWQLDLSFGC 146

RESULT 2

US-08-788-943A-5
; Sequence 5, Application US/08788943A
; Patent No. 5831017
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, James Arthur
; TITLE OF INVENTION: OBESITY PROTEIN ANALOG COMPOUNDS AND
; FORMULATIONS THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,943A
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10540
; TELEPHONE: (317) 276-0757
; TELEFAX: (317) 277-1917
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-788-943A-5

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Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 TEVVLSRLQGSQDMLWQLDLSFGC 146
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Db 121 TEVVLSRLQGSQDMLWQLDLSFGC 146

RESULT 3

US-08-823-104-3
; Sequence 3, Application US/08823104
; Patent No. 5840517
; GENERAL INFORMATION:
; APPLICANT: Atkinson, Paul R

; APPLICANT: Foster, Lisa K
; APPLICANT: Furman, Thomas C
; APPLICANT: Mackellar, Warren C
; TITLE OF INVENTION: Process for Preparing Obesity Protein
; ANALOGS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly & Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,104
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/429,362
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P
; REGISTRATION NUMBER: 36467
; REFERENCE/DOCKET NUMBER: 10022A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-8110
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 97
; OTHER INFORMATION: /note= "His at position 97 is
; OTHER INFORMATION: replaced with Gln, Asn, Ala, Gly, Ser, or Pro"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 100
; OTHER INFORMATION: /note= "Trp at position 100 is
; OTHER INFORMATION: replaced with Ala, Glu, Asp, Asn, Met, Ser, Thr, or Gly"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 101
; OTHER INFORMATION: /note= "Ala at position 101 is
; OTHER INFORMATION: replaced with Ser, Asn, Gly, His, Pro, Thr, or Val"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 102
; OTHER INFORMATION: /note= "Ser at position 102 is
; OTHER INFORMATION: replaced with Arg"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 103
; OTHER INFORMATION: /note= "Gly at position 103 is
; OTHER INFORMATION: replaced with Ala"
; FEATURE:

NAME/KEY: Modified-site
LOCATION: 105
OTHER INFORMATION: /note= "Glu at position 105 is
OTHER INFORMATION: replaced with Gln"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 106
OTHER INFORMATION: /note= "Thr at position 106 is
OTHER INFORMATION: replaced with Lys or Ser"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 107
OTHER INFORMATION: /note= "Leu at position 107 is
OTHER INFORMATION: replaced with Pro"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 111
OTHER INFORMATION: /note= "Gly at position 111 is
OTHER INFORMATION: replaced with Asp"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 118
OTHER INFORMATION: /note= "Gly at position 118 is
OTHER INFORMATION: replaced with Leu"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 138
OTHER INFORMATION: /note= "Trp at position 138 is
OTHER INFORMATION: replaced with Ala, Glu, Asp, Asn, Met, Ser, Thr, or Gly"
US-08-823-104-3

Query Match 100.0%; Score 736; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Qy 61 YQOILTSMPNSRVNIOISNDLENRLDLHLVAFPSKCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQOILTSMPNSRVNIOISNDLENRLDLHLVAFPSKCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVALSRLOGLQSLQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLQSLQDMLWQLDLSGPC 146

RESULT 4
US-09-003-081-6
; Sequence 6, Application US/09003081
; Patent No. 5968779
; GENERAL INFORMATION:
; APPLICANT: Campfield, Arthur Dr.
; APPLICANT: Devos, Rene Dr.
; APPLICANT: Guisez, Yves Dr.
; TITLE OF INVENTION: Recombinant Obese (OB) Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche, Inc.
; STREET: 340 Kingeland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,081
; FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/435,777
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Picut, Catherine A.
REGISTRATION NUMBER: 37419
REFERENCE/DOCKET NUMBER: 9165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4387
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-003-081-6
Query Match 100.0%; Score 736; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Qy 61 YQOILTSMPNSRVNIOISNDLENRLDLHLVAFPSKCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQOILTSMPNSRVNIOISNDLENRLDLHLVAFPSKCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVALSRLOGLQSLQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLQSLQDMLWQLDLSGPC 146
RESULT 5
US-08-648-262-6
; Sequence 6, Application US/08648262
; Patent No. 6025324
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal Mr.
; APPLICANT: Campfield, Arthur Dr.
; APPLICANT: Devos, Rene Dr.
; APPLICANT: Guisez, Yves Dr.
; TITLE OF INVENTION: Pegylated Obese (OB) Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche, Inc.
; STREET: 340 Kingeland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/648,262
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Epstein, William H.
; REGISTRATION NUMBER: 20008
; REFERENCE/DOCKET NUMBER: 9281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-3723
; TELEFAX: (201) 235-2363

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-648-263-6
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQOILTSMPSRNVQIISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQOILTSMPSRNVQIISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVVALSRLQGSLODMLWQLDLSGPC 146
Db 121 TEVVALSRLQGSLODMLWQLDLSGPC 146

RESULT 6
US-08-648-263-6
; Sequence 6, Application US/08648263
; Patent No. 6025325
; GENERAL INFORMATION:
; APPLICANT: Campfield, Arthur
; APPLICANT: Devos, Rene
; APPLICANT: Guisez, Yves
; TITLE OF INVENTION: RECOMBINANT OBESE (OB) PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingeland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/648,263
; FILING DATE: 15-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,629
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,777
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kreieler, Lewis J
; REGISTRATION NUMBER: 38522
; REFERENCE/DOCKET NUMBER: RAN 4105/175-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)235-4387
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown

; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-648-263-6
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQOILTSMPSRNVQIISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQOILTSMPSRNVQIISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVVALSRLQGSLODMLWQLDLSGPC 146
Db 121 TEVVALSRLQGSLODMLWQLDLSGPC 146

RESULT 7
US-08-914-375C-32
; Sequence 32, Application US/08914375C
; Patent No. 6377893
; GENERAL INFORMATION:
; APPLICANT: Steven A. Benner
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: 1501 NW 68th Terrace
; CITY: Gainesville
; STATE: FL
; COUNTRY: United States
; ZIP: 32605-4147
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,375C
; FILING DATE: 19-Aug-1997
; CLASSIFICATION: 702/20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352 392 7773
; TELEFAX: 352 331 0462
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: leptin
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
;
US-08-914-375C-32
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQOILTSMPSRNVQIISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQOILTSMPSRNVQIISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
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Db	61	YQQLTSPSRNVQISNDLENRLDHLVLA	PFKSKCHLPWASGLETTDLSGGVLEASGYS	120
Qy	121	TEVVALSRQGSIQDMLWOLDLSPG	146	
Db	121	TEVVALSRQGSIQDMLWOLDLSPG	146	

RESULT 10

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RESOLUTION 10
US-09-200-919-1
; Sequence 1, Application US/09200919
; Patent No. 6518235
; GENERAL INFORMATION:
; APPLICANT: OOMURA, YUTAKA
; APPLICANT: HORI, NOBUAKI
; APPLICANT: SHIRAISHI, TAKEMASA
; APPLICANT: SASAKI, KAZUO
; APPLICANT: TAKEDA, HIROSHI
; APPLICANT: TSUJI, MINORU
; APPLICANT: MATSUMIYA, TERUHIKO
; TITLE OF INVENTION: DRUG FOR IMPROVEMENT OF BRAIN FUNCTION
; FILE REFERENCE: YAMA-100
; CURRENT APPLICATION NUMBER: US/09/200,919
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: HUMAN
US-09-200-919-1

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PRECEDENT 11

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RESULT 11
PCT-US96-00952-2
; Sequence 2, Application PC/TUS9600952
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Obesity Proteins
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00952
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-00952-2

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Qy	121	TEVVALSRLOGSLQDMLWQLDLSPGC	146
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RESULT 8

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RE-001
US-09-172-644-1
; Sequence 1, Application US/09172644
; Patent No. 6420339
; GENERAL INFORMATION:
;
; APPLICANT: GEGG, COLIN
; APPLICANT: KINSTLER, OLAF
; TITLE OF INVENTION: SITE-DIRECTED DUAL PEGYLATION OF PROTEINS FOR IMPROVED
; TITLE OF INVENTION: BIOACTIVITY AND BIOCOMPATIBILITY
; FILE REFERENCE: A-567
; CURRENT APPLICATION NUMBER: US/09/172,644
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human Leptin
US-09-172-644-1

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RESIT.T 9

RESOL-19
US-09-221-178-1
US-09-221-178-1, Application US/09221178
; Sequence No. 6451346
; Patent No. 6451346
; GENERAL INFORMATION:
; APPLICANT: SHAH, SUBODH
; APPLICANT: DAI, WEIGUO
; APPLICANT: DAI, WEIGUO
; TITLE OF INVENTION: BIODEGRADABLE, PH/THERMOSENSITIVE HYDROGEL FOR
; TITLE OF INVENTION: SUSTAINED DELIVERY OF BIOLOGICALLY ACTIVE AGENTS
; FILE REFERENCE: A-575
; CURRENT APPLICATION NUMBER: US/09/221,178
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human Leptin
US-09-221-178-1

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	Best Local Similarity	100.0%;	Pred. No. 3.4e-74;		
	Matches 146;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	VPIQKVQDDTKTLKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV	60		
Db	1	VPIQKVQDDTKTLKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV	60		
Qy	61	YQQLITSPSRNVIQISNDLENRLDLHLVLAFAFSKCHLPWASGLETTDLDSGLGVLEASGYS	120		

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPSRNVIOISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 120
DB 61 YQOILTSMPSRNVIOISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 120

QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 121 TEVVALSRLOGLQDMLWQLDLSGPC 146

RESULT 12

PCT-US96-00952-3
; Sequence 3, Application PC/TUS9600952
; GENERAL INFORMATION:
; APPLICANT: Anti-Obesity Proteins
; TITLE OF INVENTION: Anti-Obesity Proteins
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00952
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-00952-3

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPSRNVIOISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 120
DB 61 YQOILTSMPSRNVIOISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 120

QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 121 TEVVALSRLOGLQDMLWQLDLSGPC 146

RESULT 13

US-09-200-919-4
; Sequence 4, Application US/09200919
; Patent No. 6518235
; GENERAL INFORMATION:
; APPLICANT: OOMURA, YUTAKA
; APPLICANT: HORI, NOBUAKI
; APPLICANT: SHIRAI, TAKEMASA
; APPLICANT: SASAKI, KAZUO
; APPLICANT: TAKEDA, HIROSHI
; APPLICANT: TSUJI, MINORU
; APPLICANT: MATSUMIYA, TERUHIKO
; TITLE OF INVENTION: DRUG FOR IMPROVEMENT OF BRAIN FUNCTION
; FILE REFERENCE: YAMA-100

; CURRENT APPLICATION NUMBER: US/09/200,919
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 147
; TYPE: PRT
; ORGANISM: HUMAN
; US-09-200-919-4

Query Match 100.0%; Score 736; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 3.5e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 2 VPIQKVDDTKTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 61

QY 61 YQOILTSMPSRNVIOISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 120
DB 62 YQOILTSMPSRNVIOISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 121

QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 122 TEVVALSRLOGLQDMLWQLDLSGPC 147

RESULT 14

US-08-429-362-3
; Sequence 3, Application US/08429362
; Patent No. 5614379
; GENERAL INFORMATION:
; APPLICANT: Mackellar, Warren C.
; TITLE OF INVENTION: Process For Preparing Anti-Obesity
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company/Patent Division
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,362
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P.
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0757
; TELEFAX: (317) 277-1917
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-429-362-3

Query Match 100.0%; Score 736; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.5e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Db 3 VPIQKVDQDTKTLIKTIIVTRINDISHQTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 62
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGYS 120
Db 63 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGYS 122
QY 121 TEVVALSRLQGSLOQDMWLQDLSPGC 146
Db 123 TEVVALSRLQGSLOQDMWLQDLSPGC 148

QY 121 TEVVALSRLQGSLOQDMWLQDLSPGC 146
Db 123 TEVVALSRLQGSLOQDMWLQDLSPGC 148
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Job time : 34.1134 secs

RESULT 15
US-08-823-104-18
: Sequence 18, Application US/08823104
: Patent No. 5840517
: GENERAL INFORMATION:
: APPLICANT: Atkinson, Paul R
: APPLICANT: Foster, Lisa K
: APPLICANT: Furman, Thomas C
: APPLICANT: MacKellar, Warren C
: TITLE OF INVENTION: Process for Preparing Obesity Protein
: TITLE OF INVENTION: Analogs
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Eli Lilly & Company
: STREET: Lilly Corporate Center
: CITY: Indianapolis
: STATE: Indiana
: COUNTRY: USA
: ZIP: 46285
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/823,104
: FILING DATE: 24-MAR-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/429,362
: FILING DATE: 26-APR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Caltrider, Steven P
: REGISTRATION NUMBER: 36467
: REFERENCE/DOCKET NUMBER: 10022A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 317-277-8110
: TELEFAX: 317-277-1917
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 148 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
US-08-823-104-18

Query Match 100.0%; Score 736; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.5e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDQDTKTLIKTIIVTRINDISHQTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 3 VPIQKVDQDTKTLIKTIIVTRINDISHQTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 62
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGYS 120
Db 63 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLPWASGLETLDSLGGLVLEASGYS 122

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OM protein - protein search, using sw model

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(without alignments)
540.393 Million cell updates/sec

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Perfect score: 736
Sequence: 1 VPIQKVDDTKTLIKTIVTR.....SRQGSLLQDMLWQLDLSGPC 146

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	736	100.0	146	4	US-10-139-794-10
3	736	100.0	146	4	US-10-419-058-2
4	736	100.0	146	4	US-10-467-114-1
5	736	100.0	146	4	US-10-622-998-1
6	736	100.0	146	4	US-10-658-834A-211
7	736	100.0	146	4	US-10-468-496-1
8	736	100.0	146	5	US-10-872-198-127
9	736	100.0	146	5	US-10-623-189-1
10	736	100.0	146	5	US-10-502-344-22
11	736	100.0	146	6	US-11-021-951-127
12	736	100.0	167	3	US-09-736-084-4
13	736	100.0	167	3	US-09-928-522-7
14	736	100.0	167	3	US-09-789-306-3
15	736	100.0	167	3	US-09-804-409A-11
16	736	100.0	167	3	US-09-316-393-4
17	736	100.0	167	4	US-10-440-464-67
18	736	100.0	167	4	US-10-458-334-17
19	736	100.0	167	4	US-10-730-488-4
20	736	100.0	167	4	US-10-780-295-4
21	736	100.0	167	5	US-10-723-860-2482
22	736	100.0	167	5	US-10-698-510-17
23	736	100.0	167	5	US-10-775-180-168
24	736	100.0	167	5	US-10-775-180-169
25	736	100.0	167	5	US-10-775-180-170
26	736	100.0	167	5	US-10-775-180-171
27	736	100.0	167	5	US-10-893-315-63

28	736	100.0	167	5	US-10-756-149-5381	Sequence 5381, App
29	736	100.0	167	5	US-10-775-204-551	Sequence 551, App
30	736	100.0	167	5	US-10-775-204-555	Sequence 555, App
31	736	100.0	167	5	US-10-775-204-557	Sequence 557, App
32	736	100.0	167	5	US-10-775-204-558	Sequence 558, App
33	736	100.0	167	6	US-11-060-291-1	Sequence 1, Appli
34	736	100.0	171	5	US-10-908-400A-105	Sequence 105, App
35	736	100.0	178	5	US-10-893-315-108	Sequence 108, App
36	736	100.0	374	4	US-10-679-999-15	Sequence 15, Appl
37	736	100.0	374	4	US-10-679-999-18	Sequence 18, Appl
38	736	100.0	374	6	US-11-054-085-15	Sequence 15, Appl
39	736	100.0	374	6	US-11-054-085-18	Sequence 18, Appl
40	736	100.0	379	4	US-10-679-999-9	Sequence 9, Appli
41	736	100.0	379	4	US-10-679-999-12	Sequence 12, Appl
42	736	100.0	379	6	US-11-054-085-9	Sequence 9, Appli
43	736	100.0	379	6	US-11-054-085-12	Sequence 12, Appl
44	736	100.0	396	3	US-09-859-361-2	Sequence 2, Appli
45	736	100.0	396	3	US-09-859-361-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-191-377-1
; Sequence 1, Application US/10191377
; Publication No. US20030099709A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: BIODEGRADABLE, PH/THERMOSENSITIVE HYDROGEL FOR
; FILE REFERENCE: A-575
; CURRENT APPLICATION NUMBER: US/10/191.377
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human Leptin
US-10-191-377-1

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VPIQKVDDTKTLIKTIVTRINDISHQSVSSKOKVTGLDPIGLHPLTILSKMDQTLAV	60
Db	1	VPIQKVDDTKTLIKTIVTRINDISHQSVSSKOKVTGLDPIGLHPLTILSKMDQTLAV	60
Qy	61	YQQILTSPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS	120
Db	61	YQQILTSPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS	120
Qy	121	TEVVALSRQGSLLQDMLWQLDLSGPC	146
Db	121	TEVVALSRQGSLLQDMLWQLDLSGPC	146

RESULT 2
US-10-139-794-10
; Sequence 10, Application US/10139794
; Publication No. US20030232421A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS, LYNX THERAPEUTICS INC.
; APPLICANT: Pierre Legrain, Simon Whiteside, Jen-I Mao, Irina Khrebtukova, Shujun
; TITLE OF INVENTION: Protein-Protein Interactions In Adipocyte Cells (3)
; FILE REFERENCE: B4883A
; CURRENT APPLICATION NUMBER: US/10/139,794
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/288,885
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 2930

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Translation of SEQ ID NO:9
US-10-139-794-10

Query Match      100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVLSRLQGSQDMLWQLDLSPGC 146
DB 121 TEVVLSRLQGSQDMLWQLDLSPGC 146

RESULT 3
US-10-419-058-2
; Sequence 2, Application US/10419058
; Publication No. US20040053366A1
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Zhang, Jinyang
; TITLE OF INVENTION: Expression and Export of Anti-Obesity Proteins as Fc
; TITLE OF INVENTION: Fusion Proteins
; FILE REFERENCE: LEX-008
; CURRENT APPLICATION NUMBER: US/10/419,058
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US/09/479,508
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 60/115,079
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-419-058-2

Query Match      100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVLSRLQGSQDMLWQLDLSPGC 146
DB 121 TEVVLSRLQGSQDMLWQLDLSPGC 146

RESULT 4
US-10-467-114-1
; Sequence 1, Application US/10467114
; Publication No. US20040072219A1
; GENERAL INFORMATION:
```

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; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-115
; CURRENT APPLICATION NUMBER: US/10/467,114
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102618.4
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01188
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-467-114-1

Query Match      100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVLSRLQGSQDMLWQLDLSPGC 146
DB 121 TEVVLSRLQGSQDMLWQLDLSPGC 146

RESULT 5
US-10-622-998-1
; Sequence 1, Application US/10622998
; Publication No. US20040105840A1
; GENERAL INFORMATION:
; APPLICANT: Kinstler, Olaf
; APPLICANT: Ladd, David
; APPLICANT: Papisov, Mikhail
; TITLE OF INVENTION: PROTEIN CONJUGATES WITH A WATER-SOLUBLE BIOCOMPATIBLE, BIODEGRAD
; TITLE OF INVENTION: POLYMER
; FILE REFERENCE: A-822
; CURRENT APPLICATION NUMBER: US/10/622,998
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/397,509
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-622-998-1

Query Match      100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
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Db 61 YQILTSMPNSRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
121 TEVVALSRLOGLQDMLWQLDLSGPC 146
121 TEVVALSRLOGLQDMLWQLDLSGPC 146

RESULT 6
US-10-658-834A-211
; Sequence 211, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Driantani, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAA60470
; DATABASE ENTRY DATE: 1995-01-13
US-10-658-834A-211

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
Qy 61 YQILTSMPNSRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQILTSMPNSRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Qy 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
Db 121 TEVVALSRLOGLQDMLWQLDLSGPC 146

RESULT 7
US-10-468-496-1
; Sequence 1, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19

; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-468-496-1
Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
Qy 61 YQILTSMPNSRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQILTSMPNSRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Qy 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
Db 121 TEVVALSRLOGLQDMLWQLDLSGPC 146

RESULT 8
US-10-872-198-127
; Sequence 127, Application US/10872198
; Publication No. US2005002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHREIDIG
; APPLICANT: Christian VOETSMEIER
; APPLICANT: Ulrich Ketting
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U4
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-127

Query Match 100.0%; Score 736; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.3e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VPIQKVQDDTKLIIKTIIVTRINDISHTSQSVSSKQKVTGLDFIPGLHPILITLSKMOOTLAV	60
Db	1	VPIQKVQDDTKLIIKTIIVTRINDISHTSQSVSSKQKVTGLDFIPGLHPILITLSKMOOTLAV	60
Qy	61	YQOILTSPMSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGY	120
Db	61	YQOILTSPMSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGY	120
Qy	121	TEVVALSRLOGLSQDMLWOLDLSPGC	146
Db	121	TEVVALSRLOGLSQDMLWOLDLSPGC	146

RESULT 9
US-10-623-189-1
; Sequence 1, Application US/10623189
; Publication No. US20050020496A1
; GENERAL INFORMATION:
; APPLICANT: DEPAOLI, Alex M.
; APPLICANT: ORAL, Elif Arioglu
; APPLICANT: TAYLOR, Simeon I.
; APPLICANT: GARG, Abhimanyu
; TITLE OF INVENTION: USE OF LEPTIN FOR TREATING HUMAN LIPOATROPHY AND METHOD OF DETERM
; TITLE OF INVENTION: PREDISPOSITION TO SAID TREATMENT
; FILE REFERENCE: 54113.8005.US02
; CURRENT APPLICATION NUMBER: US/10/623,189
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 10/279,129
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 60/336,394
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 146
; TYPE: ERT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Leptin Human 146 (rHu-Leptin 1-146)
US-10-623-189-1

RESULT 10
US-10-502-344-22
: Sequence 22, Application US/10502344
: Publication No. US20050214762A1
: GENERAL INFORMATION:
: APPLICANT: ROSS, Richard
: APPLICANT: ARTYMIUK, Peter
: APPLICANT: SAYERS, Jon
: TITLE OF INVENTION: Polypeptide Variants
: FILE REFERENCE: 100042.55084US
: CURRENT APPLICATION NUMBER: US/10/502,344
: CURRENT FILING DATE: 2004-07-23
: PRIOR APPLICATION NUMBER: PCT/GB03/00253
: PRIOR FILING DATE: 2003-01-24
: PRIOR APPLICATION NUMBER: GB 0201679.8

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RESULT 11
US-11-021-951-127
; Sequence 127, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMEIER, Christian
; APPLICANT: Ketting, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.0002U5
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-127

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QY 61 YQILTSMPNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB ||||||||||||||||||
QY 61 YQILTSMPNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB ||||||||||||||||||
QY 121 TEVVALSRQGSLODMLWQLDLSGPC 146
DB ||||||||||||||||||
QY 121 TEVVALSRQGSLODMLWQLDLSGPC 146
DB ||||||||||||||||||

RESULT 12
US-09-736-084-4
; Sequence 4, Application US/09736084
; Patent No. US20020107211A1
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/736,084
; FILING DATE: 13-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. US20020107211A1 member 30, 1994
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-736-084-4

Query Match 100.0%; Score 736; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 5.1e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60
DB ||||||||||||||||||
QY 22 VPIQKVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 81
DB ||||||||||||||||||
QY 61 YQILTSMPNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB ||||||||||||||||||
QY 82 YQILTSMPNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 141
DB ||||||||||||||||||

QY 121 TEVVALSRQGSLODMLWQLDLSGPC 146
DB ||||||||||||||||||
QY 142 TEVVALSRQGSLODMLWQLDLSGPC 167
DB ||||||||||||||||||
RESULT 13
US-09-928-522-7
; Sequence 7, Application US/09928522
; Patent No. US20020110857A1
; GENERAL INFORMATION:
; APPLICANT: Spurlock, Michael E.
; TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID
; SEQUENCES CODING THEREFOR AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYTHE HIRSCHBOECK DUDEK S.C.
; STREET: Suite 2100 111 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/928,522
; FILING DATE: 13-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,908
; FILING DATE: 31-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Florecher, Gary R.
; REGISTRATION NUMBER: 27,830
; REFERENCE/DOCKET NUMBER: PM-8808
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 414-273-2100
; TELEFAX: 414-223-5000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-928-522-7

Query Match 100.0%; Score 736; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 5.1e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60
DB ||||||||||||||||||
QY 22 VPIQKVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 81
DB ||||||||||||||||||
QY 61 YQILTSMPNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB ||||||||||||||||||
QY 82 YQILTSMPNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 141
DB ||||||||||||||||||
QY 121 TEVVALSRQGSLODMLWQLDLSGPC 146
DB ||||||||||||||||||
QY 142 TEVVALSRQGSLODMLWQLDLSGPC 167
DB ||||||||||||||||||

RESULT 14
US-09-789-306-3
; Sequence 3, Application US/09789306
; Patent No. US20020142456A1
; GENERAL INFORMATION:
; APPLICANT: Hernday, Natasha

;;
;; TITLE OF INVENTION: Canine OB Protein Compositions and
;; Methods
;;
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Angen Inc.
;; STREET: One Angen Center Drive
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 91320
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/789,306
;; FILING DATE: 20-Feb-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/609,408
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Eggert, Joan D.
;; REFERENCE/DOCKET NUMBER: A-387
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 167 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Leader Sequence
;; LOCATION: -21 to -1
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-789-306-3

Query Match 100.0%; Score 736; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 5.le-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
|||
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
|||

QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120
|||
Db 82 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 141
|||

QY 121 TEVVLSRLQGSLODMWLQDLSPGC 146
|||
Db 142 TEVVLSRLQGSLODMWLQDLSPGC 167
|||

RESULT 15
US-09-804-409A-11
; Sequence 11, Application US/09804409A
; Patent No. US20020155100A1
; GENERAL INFORMATION:
; APPLICANT: KIEFFER, TIMOTHY J.
; APPLICANT: CHEUNG, ANTHONY T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
; FILE OF INVENTION: EXPRESSION IN GUT
; FILE REFERENCE: 029996/027 8721
; CURRENT APPLICATION NUMBER: US/09/804,409A
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 11
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-804-409A-11

Query Match 100.0%; Score 736; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 5.le-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
|||
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
|||

QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120
|||
Db 82 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 141
|||

QY 121 TEVVLSRLQGSLODMWLQDLSPGC 146
|||
Db 142 TEVVLSRLQGSLODMWLQDLSPGC 167
|||

Search completed: May 4, 2006, 22:02:16
Job time : 112.887 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:58:39 ; Search time 18.0619 Seconds
(without alignments)
374.135 Million cell updates/sec

Title: US-10-623-189-1
Perfect score: 736
Sequence: 1 VPIQKVQDDTKTLTKTIVTR.....SRLOGLQDMLWOLDLSPGC 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
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11: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB_PUB.pep1.*
12: /SIDSS5/ptodata/2/pubpaa/US60_NEW_PUB_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	146	9	US-10-519-390-19
2	736	100.0	146	11	US-11-176-830-211
3	736	100.0	167	11	US-11-236-198-32
4	736	100.0	185	9	US-10-821-234-1384
5	736	100.0	397	11	US-11-192-219-47
6	734	99.7	146	11	US-11-176-830-666
7	734	99.7	146	11	US-11-176-830-672
8	734	99.7	146	11	US-11-176-830-677
9	734	99.7	146	11	US-11-176-830-683
10	733	99.6	146	11	US-11-176-830-665
11	733	99.6	146	11	US-11-176-830-671
12	733	99.6	146	11	US-11-176-830-673
13	733	99.6	146	11	US-11-176-830-676
14	733	99.6	146	11	US-11-176-830-682
15	733	99.6	146	11	US-11-236-198-36
16	731	99.3	146	11	US-11-176-830-674
17	731	99.3	146	11	US-11-176-830-675
18	731	99.3	146	11	US-11-176-830-679
19	731	99.3	146	11	US-11-176-830-681
20	730	99.2	146	11	US-11-176-830-678
21	730	99.2	146	11	US-11-176-830-680

ALIGNMENTS

RESULT 1

US-10-519-390-19
Sequence 19, Application US/10519390
Publication No. US2006008872A1

GENERAL INFORMATION:

APPLICANT: MEDEXGEN Inc.

APPLICANT: CHUNG, Yong-Hoon

APPLICANT: LEE, Hak-sup

APPLICANT: YI, Ki-Wan

APPLICANT: KIM, Jae-Youn

APPLICANT: HEO, Youn-Hwa

TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

TITLE OF INVENTION: proteins and the example mutants

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/519,390

CURRENT FILING DATE: 2004-12-23

PRIOR APPLICATION NUMBER: KR10-2003-0051846

PRIOR FILING DATE: 2003-07-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Kopatentin 1.71

SEQ ID NO 19

LENGTH: 146

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: LPT: 41st or 92nd Phe is replaced by Val.

US-10-519-390-19

Query Match 100.0%; Score 736; DB 9; Length 146;

Best Local Similarity 100.0%; Pred. No. 2.4e-65;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLTKTIVTRINDISHTQSVSSKQKVTGLDPIPGHPIITLSKMDQTLAV 60

Db 1 VPIQKVQDDTKTLTKTIVTRINDISHTQSVSSKQKVTGLDPIPGHPIITLSKMDQTLAV 60

Qy 61 YQQLTSMPSRNVQISNDLENLDLHLVAFSKCHLPWASGLTDLGLGVLEASGYS 120

Db 61 YQQLTSMPSRNVQISNDLENLDLHLVAFSKCHLPWASGLTDLGLGVLEASGYS 120

Qy 121 TEVVALSRLOGLQDMLWOLDLSPGC 146

Db 121 TEVVALSRLOGLQDMLWOLDLSPGC 146

Sequence 663, App
Sequence 664, App
Sequence 667, App
Sequence 668, App
Sequence 31, Appl
Sequence 5, Appl
Sequence 670, App
Sequence 669, App
Sequence 37, Appl
Sequence 33, Appl
Sequence 28, Appl
Sequence 39, Appl
Sequence 35, Appl
Sequence 34, Appl
Sequence 8, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 54, Appl

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RESULT 2
US-11-176-830-211
; Sequence 211, Application US/11176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; FILE OF INVENTION: Acid Molecules and Related Applications
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAA60470
; DATABASE ENTRY DATE: 1995-01-13
US-11-176-830-211

Query Match 100.0%; Score 736; DB 11; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.4e-65;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
QY 121 TEVVALSRQGSLODMWLQDLSPGC 146
DB 121 TEVVALSRQGSLODMWLQDLSPGC 146

RESULT 3
US-11-236-198-32
; Sequence 32, Application US/11236198
; Publication No. US20060030530A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Fruebis, Joachim
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
; FILE REFERENCE: 70 US2,REG
; CURRENT APPLICATION NUMBER: US/11/236,198
; CURRENT FILING DATE: 2005-09-27
; PRIOR APPLICATION NUMBER: US/09/668,558
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,506
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent.pm
; SEQ ID NO 32
; LENGTH: 167
; TYPE: PRT

Query Match 100.0%; Score 736; DB 11; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.4e-65;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
QY 121 TEVVALSRQGSLODMWLQDLSPGC 146
DB 121 TEVVALSRQGSLODMWLQDLSPGC 146

RESULT 4
US-10-821-234-1384
; Sequence 1384, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1384
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1384

Query Match 100.0%; Score 736; DB 9; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.2e-65;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 40 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 99
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 100 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 159
QY 121 TEVVALSRQGSLODMWLQDLSPGC 146
DB 160 TEVVALSRQGSLODMWLQDLSPGC 185

RESULT 5
US-11-192-219-47
; Sequence 47, Application US/11192219
; Publication No. US20050272656A1
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; TITLE OF INVENTION: USES FOR WSX LIGANDS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
```

```
; ORGANISM: Homo sapiens
US-11-236-198-32

Query Match 100.0%; Score 736; DB 11; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.8e-65;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 82 YQQLTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 141
QY 121 TEVVALSRQGSLODMWLQDLSPGC 146
DB 142 TEVVALSRQGSLODMWLQDLSPGC 167
```

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/192,219
FILING DATE: 27-Jul-2005
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/667,197
FILING DATE: 20-Jun-1996
APPLICATION NUMBER: 08/585005
FILING DATE: 08-Jan-96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: P-40,378
REFERENCE/DOCKET NUMBER: P0986P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-11-192-219-47

Query Match 100.0%; Score 736; DB 11; Length 397;
Best Local Similarity 100.0%; Pred. No. 8.8e-65;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
Qy 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSGGVLEASGY 120
Db 82 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSGGVLEASGY 141
Qy 121 TEVVALSRLOGLQDMLWQDLSPGC 146
Db 142 TEVVALSRLOGLQDMLWQDLSPGC 167

RESULT 6
US-11-176-830-666
; Sequence 666, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; FILE OF INVENTION: Acid Molecules and Related Applications
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 666
; LENGTH: 146

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-666
Query Match 99.7%; Score 734; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 3.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSGGVLEASGY 120
Db 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSGGVLEASGY 120
Qy 121 TEVVALSRLOGLQDMLWQDLSPGC 146
Db 121 TEVVALSRLOGLQDMLWQDLSPGC 146

RESULT 7

US-11-176-830-672
; Sequence 672, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; FILE OF INVENTION: Acid Molecules and Related Applications
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 672
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-672

Query Match 99.7%; Score 734; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 3.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSGGVLEASGY 120
Db 61 YQQLTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDLSGGVLEASGY 120
Qy 121 TEVVALSRLOGLQDMLWQDLSPGC 146
Db 121 TEVVALSRLOGLQDMLWQDLSPGC 146

RESULT 8

US-11-176-830-677
; Sequence 677, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry

; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 677
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-677

Query Match 99.7%; Score 734; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 3.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
QY 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVALSRLOGSLODMLWQLDLSPGC 146
DB 121 TEVVALSRLOGSLODMLWQLDLSPGC 146

RESULT 9
US-11-176-830-683
; Sequence 683, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 683
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-683

Query Match 99.7%; Score 734; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 3.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60

QY 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
QY 121 TEVVALSRLOGSLODMLWQLDLSPGC 146
DB 121 TEVVALSRLOGSLODMLWQLDLSPGC 146

RESULT 10
US-11-176-830-665
; Sequence 665, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 665
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-665

Query Match 99.6%; Score 733; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 4.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
QY 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVALSRLOGSLODMLWQLDLSPGC 146
DB 121 TEVVALSRLOGSLODMLWQLDLSPGC 146

RESULT 11
US-11-176-830-671
; Sequence 671, Application US/11/176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21


```

; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 671
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-671

```

Query Match	99.6%;	Score 733;	DB 11;	Length 146;
Best Local Similarity	99.3%;	Pred. No. 4.7e-65;		
Matches 145;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	VPIQKVDDDKTLIKTIVTRINDISHTQSVSSKOKVTGLDFIPGLHPILTLTKMDQTLAV	60	
Db	1	VPIQKVDDDKTLIKTIVTRINDISHTQSVSSKOKVTGLDFIPGLHPILTLTKMDQTLAV	60	
Qy	61	YQOILTSMPSRNVQISNDLENRLDLHLVLAFSKSLPWAASGVIETLDSLGGVLEASGYS	120	
Db	61	YQOILTSMPSRNVQISNDLENRLDLHLVLAFSKSLPWAASGVIETLDSLGGVLEASGYS	120	
Qy	121	TEVVALSRLOGSLODMLWOLDLSPGC	146	
Db	121	TEVVALSRLOGSLODMLWOLDLSPGC	146	

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RESULT 12
US-11-176-830-673
; Sequence 673, Application US/11176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid Molecules and Related Applications
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/458,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 673
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-176-830-673

```

[illegible]

RESULT 13

```

US-11-176-830-676
; Sequence 676, Application US/11/176830
; Publication No. US20060030116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of
; TITLE OF INVENTION: Acid Molecules and R
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176.830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 676
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-676

```

	Query Match	99.6%	Score 733;	DB 11;	Length 146;
	Best Local Similarity	99.3%	Pred. No. 4.7e-65;		
	Matches 145;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	VPIQKVODDFTKLITVTRINDISHTQSVSSKQKVGTGLDFIPGLHPILTILSKMDQTLAV	60		
Db	1	VPIQKVODDFTKLITVTRINDISHTQSVSSKQKVGTGLDFIPGLHPILTILSKMDQTLAV	60		
Qy	61	YQOILTSMPSRNVQISNDLENRLDLHLVLAFSKSLPWAASGLTLDLSGLGVLEASGYS	120		
Db	61	YQOILTSMPSRNVQISNDLENRLDLHLVLAFSKSLPWAASGLTVDLSGLGVLEASGYS	120		
Qy	121	TEVVALSRLQGSLODMLWQLDLSPGC	146		
Db	121	TEVVALSRLQGSLODMLWQLDLSPGC	146		

```

RESULT 14
US-11-176-830-682
; Sequence 682, Application US/11176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gancier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of
; TITLE OF INVENTION: Acid Molecules and R
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 682
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-682

```

```

Query Match
99.6%; Score 733; DB 11; Length 146;

```

Best Local Similarity 99.3%; Pred. No. 4.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
-Qy 1 VPIQKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVVALSRQGSLODMLWQLDLSGPC 146
Db 121 TEVVALSRQGSLODMLWQLDLSGPC 146

RESULT 15
US-11-236-198-36
; Sequence 36, Application US/11236198
; Publication No. US20060030530A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Fruebis, Joachim
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
; FILE REFERENCE: 70.US2.REG
; CURRENT APPLICATION NUMBER: US/11/236,198
; PRIOR FILING DATE: 2005-09-27
; PRIOR APPLICATION NUMBER: US/09/668,558
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,506
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent.pm
; SEQ ID NO 36
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-11-236-198-36

Query Match 99.6%; Score 733; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 4.7e-65;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVVALSRQGSLODMLWQLDLSGPC 146
Db 121 TEVVALSRQGSLODMLWQLDLSGPC 146

Search completed: May 4, 2006, 22:02:58
Job time : 19.0619 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:46:23 ; Search time 137.526 Seconds
(without alignments)
463.258 Million cell updates/sec

Title: US-10-623-189-2

Perfect score: 731

Sequence: 1 VPIQKVQDDTKTLTIIVTR.....SRLQSLQDMLQQLDLSGCC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	731	100.0	145	2 AAW00302	Aaw00302 Human del
2	731	100.0	145	2 AAW00541	Aaw00541 Human mat
3	731	100.0	145	2 AAW30893	Aaw30893 Synthetic
4	731	100.0	145	3 AAY92815	Aay92815 Mature le
5	731	100.0	145	3 AAY83769	Aay83769 Human OB
6	731	100.0	145	3 AAY97889	Aay97889 Mutant ma
7	731	100.0	145	3 AAY95787	Aay95787 Mature re
8	731	100.0	145	3 AAB14266	Aab14266 Mature hu
9	731	100.0	145	6 ABR57163	Abr57163 Recombina
10	731	100.0	146	2 AAW34397	Aaw34397 Human Met
11	731	100.0	146	3 AAY97890	Aay97890 Mutant ma
12	731	100.0	146	3 AAY92262	Aay92262 Mature re
13	731	100.0	165	2 AAW00537	Aaw00537 Human obe
14	731	100.0	166	2 AAW00515	Aaw00515 Human obe
15	731	100.0	166	2 AAW00525	Aaw00525 Human obe
16	731	100.0	166	2 AAW00530	Aaw00530 Human obe
17	731	100.0	166	2 AAW00532	Aaw00532 Human obe
18	731	100.0	166	2 AAW00531	Aaw00531 Human obe
19	731	100.0	166	2 AAW00523	Aaw00523 Human obe
20	731	100.0	166	2 AAW00533	Aaw00533 Human obe
21	731	100.0	166	3 AAB28450	Aab28450 Human OB
22	731	100.0	166	3 AAY87728	Aay87728 Murine OB
23	731	100.0	166	3 AAB28469	Aab28469 Human OB
24	731	100.0	166	5 AABG74166	Abg74166 Human obe

ALIGNMENTS

RESULT 1

AAW00302

ID AAW00302 standard; protein; 145 AA.

XX

AC AAW00302;

XX

DT 20-NOV-1996 (first entry)

XX

DE Human delta Gln28 ob protein.

XX

KW Human; obesity protein; ob; fat cell cDNA library; primer; PCR;
polymerase chain reaction; amplify; dipeptide leader; antibody;
peripheral adipose tissue; weight gain; obese; peptide hormone;
fat deposit; type II diabetes; cardiovascular disease; cancer.

OS Homo sapiens.

XX

PN WO9624670-A1.

XX

PD 15-AUG-1996.

XX

PF 29-JAN-1996; 96WO-US001411.

XX

PR 06-FEB-1995; 95US-00384493.

XX

PA 26-MAY-1995; 95US-00451250.

XX

(ELIL) LILLY & CO ELI.

PI

Basinski MB, Schoner BE;

XX

DR WPI; 1996-384442/38.

XX

N-PSDB; AAT40259, AAT40260.

XX

XX

New DNA encoding two forms of the human obesity gene product - and

XX

PS Claim 4; Page 23; 30pp; English.

XX

The sequences given in AAW00301-02 represent two forms of the human obesity protein, ob, in which Ala27Gln28 in AAW00301 are replaced by a single Thr in AAW00302. The nucleic acid sequences were isolated from a human fat cell cDNA library using the primer sequences given in AAT40261-64. The ob proteins are pref. expressed with a dipeptide leader sequence of Met-Arg or Met-Tyr. Experiments have suggested that the ob proteins are released by peripheral adipose tissue and are capable of controlling weight gain in normal and obese mice. The ob proteins are thought to be

Abb84118 Truncated
Abu4563 Human ob
Adt93139 Human ob
Abb84141 Truncated
Abb84140 Truncated
Abb84139 Truncated
Abb84139 Human Met
Aaw00013 Acid stab
Aar99490 Chimeric
Aaw00539 Human mat
Aaw30892 Synthetic
Aaw34482 Human obe
Aaw08595 Properly
Aaw28896 Biologica
Aaw08599 Properly
Aaw10151 Properly
Aaw22900 Biologica
Aaw22901 Biologica
Aaw30791 Obesity p
Aaw26191 Obesity p
Aaw26194 Obesity p

25 731 100.0 166 5 ABB84118
26 731 100.0 166 6 ABU4563
27 731 100.0 166 8 ADT93139
28 727 99.5 166 5 ABB84141
29 727 99.5 166 5 ABB84140
30 727 99.5 166 5 ABB84139
31 726 99.3 146 2 AAW34396
32 720.5 98.6 146 2 AAW00013
33 720.5 98.6 146 2 AAR99490
34 720.5 98.6 146 2 AAW00539
35 720.5 98.6 146 2 AAW30892
36 720.5 98.6 146 2 AAW34482
37 720.5 98.6 146 2 AAW08595
38 720.5 98.6 146 2 AAW28896
39 720.5 98.6 146 2 AAW08599
40 720.5 98.6 146 2 AAW10151
41 720.5 98.6 146 2 AAW22900
42 720.5 98.6 146 2 AAW22901
43 720.5 98.6 146 2 AAW30791
44 720.5 98.6 146 2 AAW26191
45 720.5 98.6 146 2 AAW26194

CC circulating peptide hormones which regulate the size of a bodies fat
 CC deposits. They can be used to treat obesity and to reduce the risk of
 CC type II diabetes, cardiovascular disease and cancer. Anti-ob protein
 CC antibodies may be used for diagnostic purposes

XX SQ Sequence 145 AA;

Query Match 100.0%; Score 731; DB 2; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.8e-72;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60

Db 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60

QY 61 QQILTSMPSRNVQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120

Db 61 QQILTSMPSRNVQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120

QY 121 EVVALSRLOGLQDMLWQLDLSFGC 145

Db 121 EVVALSRLOGLQDMLWQLDLSFGC 145

RESULT 2

AAW00541
 ID AAW00541 standard; protein; 145 AA.

XX AC AAW00541;

XX DT 13-SEP-1996 (first entry)

XX DE Human mature obesity protein variant.

XX KW Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
 KW food intake; energy expenditure; high blood pressure; cholesterol; human;
 KW gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.

XX OS Homo sapiens.

XX PN GB2292382-A.

XX PD 21-FEB-1996.

XX PF 17-AUG-1995; 95GB-00016947.

XX PR 17-AUG-1994; 94US-00292345.

XX PR 30-NOV-1994; 94US-00347563.

XX PR 10-MAY-1995; 95US-00438431.

XX PR 07-JUN-1995; 95US-00483211.

XX PA (UYRQ) UNIV ROCKEFELLER.

XX PI Friedman JM, Zhang Y, Proenca R, Maffei M, Halasa JL, Gajiwala K;

XX PI Burley SK;

XX DR WPI; 1996-099009/11.

XX PT Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
 PT reducing wt. in treatment of diabetes, high blood pressure and high
 PT cholesterol and for cosmetic reasons.

XX PS Claim 11; Page ?; 304pp; English.

XX CC AAW00538-W00541 represent the mature proteins of the murine and human
 CC obesity polypeptides (OBP) (full length sequences represented by AAR92719
 CC and AAR92720). OBP (also known as leptin) is a hormone involved in the
 CC regulation of body weight. This sequence has effects on both food intake
 CC and energy expenditure. OBP and its analogues are useful for modifying
 CC body weight (optionally combined with known medicaments), for treating
 CC diabetes, high blood pressure or high cholesterol. The DNA encoding this
 CC sequence (and sequences complementary to it) can be used in gene therapy
 CC for modifying body weight. This protein can be used for reducing weight

CC for health or cosmetic reasons in obese humans, or to produce leaner food
 CC animals. Antagonists of OBP (including antibodies) are useful for
 CC increasing body weight, e.g. for treating weight loss associated with
 CC cancer, or for cosmetic reasons in humans, or for production of Kobe beef
 CC or Foie gras in domestic animals. OBP antibodies (Ab) can also be used in
 CC diagnostic immunoassays for the presence of OBP. The formation of Ab-OBP
 CC complexes enables in vitro evaluation of levels of OBP in a sample,
 CC especially to detect diseases associated with elevated or decreased
 CC levels, and to monitor treatment of these diseases

XX SQ Sequence 145 AA;

Query Match 100.0%; Score 731; DB 2; Length 145;

Best Local Similarity 100.0%; Pred. No. 1.8e-72;

Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60

Db 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60

QY 61 QQILTSMPSRNVQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120

Db 61 QQILTSMPSRNVQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120

QY 121 EVVALSRLOGLQDMLWQLDLSFGC 145

Db 121 EVVALSRLOGLQDMLWQLDLSFGC 145

RESULT 3

AAW30893

ID AAW30893 standard; protein; 145 AA.

XX AC AAW30893;

XX DT 20-APR-1998 (first entry)

XX DE Synthetic obesity protein.

XX KW Obesity protein; sucrose; trehalose; treatment; obesity; diabetes;
 KW cardiovascular disease; cancer.

XX OS Synthetic.

XX PN EP797999-A2.

XX PD 01-OCT-1997.

XX PF 24-MAR-1997; 97EP-00301995.

XX PR 26-MAR-1996; 96US-0014177P.

XX PR 05-APR-1996; 96US-0014951P.

XX PA (ELIL) LILLY & CO ELI.

XX PI Beals JM, Edwards MJ, Pikal MJ, Rinella JV;

XX DR WPI; 1997-472913/44.

XX PT Pharmaceutical compositions comprising obesity protein - and sucrose
 PT and/or trehalose.
 XX PS Claim 3; Page 44-45; 48pp; English.

XX CC A novel pharmaceutical composition comprises an obesity protein, e.g. the
 CC present sequence, together with sucrose and/or trehalose. The composition
 CC can be used to treat obesity and associated disorders, e.g. diabetes,
 CC cardiovascular disease and cancer. The composition is stable and easy to
 CC manufacture

XX SQ Sequence 145 AA;

Query Match 100.0%; Score 731; DB 2; Length 145;

Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQVQDDTKTLTKTIIVTRINDISHTSVSSKQKVTGLDPIGLHPILTLTKMDOTLAVY 60
Db 1 VPIQVQDDTKTLTKTIIVTRINDISHTSVSSKQKVTGLDPIGLHPILTLTKMDOTLAVY 60

Qy 61 QQILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120
Db 61 QQILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120

Qy 121 EVVALSRQSLQDMLWOLDLSPGC 145
Db 121 EVVALSRQSLQDMLWOLDLSPGC 145

RESULT 4
AAY92815
ID AAY92815 standard; protein; 145 AA.
XX AC AAY92815;
XX DT 29-AUG-2000 (first entry)
XX DE Mature leptin receptor agonist analogue.
XX KW Leptin; analogue; lean body mass; receptor; ligand; agonist; inhibitor;
XX KW anorexia; malnutrition; cachexia; animal husbandry; immunomodulator;
XX KW catabolic.
OS Homo sapiens.
OS OS
XX Synthetic.

Key Location/Qualifiers
FT Misc-difference 4 /note= "can be replaced with Glu"
FT Misc-difference 7 /note= "can be replaced with Glu"
FT Misc-difference 22 /note= "can be replaced with Glu"
FT Misc-difference 27 /note= "can be replaced with Gln or Asp"
FT Misc-difference 27 /note= "can be replaced with Ala"
FT Misc-difference 33 /note= "can be replaced with Glu"
FT Misc-difference 53 /note= "can be replaced with methionine sulfoxide, Leu,
FT Ile, Val, Ala or Gly"
FT Misc-difference 55 /note= "can be replaced with Glu"
FT Misc-difference 61 /note= "can be replaced with Glu"
FT Misc-difference 62 /note= "can be replaced with Glu"
FT Misc-difference 67 /note= "can be replaced with Glu"
FT Misc-difference 71 /note= "can be replaced with methionine sulfoxide, Leu,
FT Ile, Val, Ala or Gly"
FT Misc-difference 74 /note= "can be replaced with Gln, Glu or Asp"
FT Misc-difference 74 /note= "can be replaced with Glu"
FT Misc-difference 76 /note= "can be replaced with Ala"
FT Misc-difference 77 /note= "can be replaced with Gln or Asp"
FT Misc-difference 81 /note= "can be replaced with Gln or Asp"
FT Misc-difference 96 /note= "can be replaced with Gln, Asn, Ala, Gly, Ser or
FT Pro"
FT Misc-difference 99 /note= "can be replaced with Ala, Glu, Asp, Asn, Met,
FT Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
FT Misc-difference 100

FT /note= "can be replaced with Ser, Asn, Gly, His, Pro, Thr
or Val"
FT Misc-difference 101 /note= "can be replaced with Arg"
FT Misc-difference 102 /note= "can be replaced with Ala"
FT Misc-difference 104 /note= "can be replaced with Gln"
FT Misc-difference 105 /note= "can be replaced with Lys or Ser"
FT Misc-difference 106 /note= "can be replaced with Pro"
FT Misc-difference 107 /note= "can be replaced with Glu"
FT Misc-difference 110 /note= "can be replaced with Asp"
FT Misc-difference 117 /note= "can be replaced with Leu"
FT Misc-difference 129 /note= "can be replaced with Glu"
FT Misc-difference 133 /note= "can be replaced with Glu"
FT Misc-difference 135 /note= "can be replaced with methionine sulfoxide, Leu,
Ile, Val, Ala or Gly"
FT Misc-difference 137 /note= "can be replaced with Ala, Glu, Asp, Asn, Met,
Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
FT Misc-difference 138 /note= "can be replaced with Glu"
XX WO200024418-A1.
XX PN
XX PD 04-MAY-2000.
XX PF 27-OCT-1999; 99WO-US025120.
XX PR 27-OCT-1998; 98US-00179461.
XX PA (ELIL) LILLY & CO BLI.
XX PI Heiman ML, Tinsley FC, Caro JF;
XX DR WPI; 2000-350589/30.
XX PT Method for preventing the loss of lean tissue mass useful in therapy
FT during catabolic states such as cachexia resulting from illnesses such as
FT anorexia and malnutrition.
XX Claim 4; Page 16; 43pp; English.
XX Leptin analogues comprise this sequence having at least one substitution
CC as featured above. A glutamine residue may be present at position 28 (see
CC AA92712) or absent as in this sequence. A claimed method for preventing
CC the loss of lean tissue mass associated with improper nutrition comprises
CC administering to a mammal a leptin receptor ligand. The leptin receptor
CC ligand is preferably a human leptin receptor agonist, such as the present
CC sequence. Binding of the leptin receptor inhibitor leads to an increase
CC of leptin production and a consequent increase in body mass. The method
CC can be used for therapy in catabolic states such as cachexia resulting
CC from illnesses such as anorexia and malnutrition. Methods of increasing
CC lean tissue growth are also useful in the fields of veterinary science
CC and animal husbandry in benefiting the health and quality of livestock
XX Sequence 145 AA;
SQ Query Match 100.0%; Score 731; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQVQDDTKTLTKTIIVTRINDISHTSVSSKQKVTGLDPIGLHPILTLTKMDOTLAVY 60
Db 1 VPIQVQDDTKTLTKTIIVTRINDISHTSVSSKQKVTGLDPIGLHPILTLTKMDOTLAVY 60

QY 61 QQILTSMPSRNVQISNDLENRLDLHLVLAFAFSKSLPWPASGLETLDSLGVLASGYST 120
 Db 61 QQILTSMPSRNVQISNDLENRLDLHLVLAFAFSKSLPWPASGLETLDSLGVLASGYST 120
 QY 121 EVVALSRLOGSLQDMLWQLDLSGPC 145
 Db 121 EVVALSRLOGSLQDMLWQLDLSGPC 145

RESULT 5
 AAY83769
 ID AAY83769 standard; protein; 145 AA.
 XX
 AC AAY83769;
 XX
 DT 21-JUN-2000 (first entry)
 XX
 DE Human OB mutein (Val22-Cys167-delta(Gln49)).
 XX
 KW Antidiabetic; anorectic; antilipemic; dextran-leptin conjugate; human;
 mature OB protein; weight modulation; diabetes; blood lipid reduction;
 hyperlipidemia; lean body mass; insulin sensitivity; heart surgery;
 liposuction; mutein.
 KW
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WO200009165-A1.
 XX
 XX 24-FEB-2000.
 XX
 XX 10-AUG-1999; 99WO-US018129.
 XX
 XX 10-AUG-1998; 98US-0096194P.
 PR 09-AUG-1999; 99US-00370684.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Litzinger DC;
 PI
 XX WPI; 2000-224187/19.
 DR
 XX
 XX
 XX New dextran-like conjugate compositions having improved efficacy and
 PT circulation time, increased solubility, and reduction in injection site
 PT reactions compared to native human leptin.
 XX
 XX
 PS Claim 8; Page; 52pp; English.
 XX
 XX The invention relates to a novel dextran-leptin conjugate comprising at
 CC least one low molecular dextran moiety, of 1-20 kDa, attached to at least
 CC one leptin moiety. The leptin moiety is preferably the mature human OB
 CC protein (AAY83768). That sequence corresponds to amino acids Val(22) to
 CC Cys(167) of the human OB protein. Alternatively the leptin may be a
 CC homologue of the human OB protein. This sequence corresponds to the
 CC Val(22)-Cys167 with the Gln49 (position 28 of AAY83768) deleted. The
 CC dextran-leptin conjugates can be used for weight modulation, treatment or
 CC prevention of diabetes, especially Type II, blood lipid reduction, e.g.
 CC hyperlipidemia, increasing lean body mass and increasing insulin
 CC sensitivity. The conjugates may also be used in combination therapies,
 CC e.g. prior to heart surgery or liposuction. The dextran-leptin conjugates
 CC have improved efficacy, longer plasma circulation time, and no kidney
 CC vacuole formation. They also have improved solubility and minimal
 CC injection site reactions. (Note: this sequence is not given in the
 CC specification but is generated from information given by the inventors)
 XX
 XX Sequence 145 AA;
 SQ

Query Match 100.0%; Score 731; DB 3; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.8e-72;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQVKTGLDFIPGLHPILTLKMDQTLAVY 60

Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQVKTGLDFIPGLHPILTLKMDQTLAVY 60
 QY 61 QQILTSMPSRNVQISNDLENRLDLHLVLAFAFSKSLPWPASGLETLDSLGVLASGYST 120
 Db 61 QQILTSMPSRNVQISNDLENRLDLHLVLAFAFSKSLPWPASGLETLDSLGVLASGYST 120
 QY 121 EVVALSRLOGSLQDMLWQLDLSGPC 145
 Db 121 EVVALSRLOGSLQDMLWQLDLSGPC 145

RESULT 6
 AAY97889
 ID AAY97889 standard; protein; 145 AA.
 XX
 AC AAY97889;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Mutant mature human leptin, delta-Q28.
 XX
 KW Leptin analogue; human; polyethylene glycol; site-specific PEGylation;
 obesity; anorectic; type II diabetes; antidiabetic; hyperlipidaemia;
 antilipaeamic; mutant; mutein.
 KW
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WO2000021574-A2.
 XX
 XX 20-APR-2000.
 XX
 XX 13-OCT-1999; 99WO-US024401.
 XX
 XX 14-OCT-1998; 98US-00172644.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Gegg C, Kinastler O;
 PI
 XX WPI; 2000-329085/28.
 DR
 XX
 XX
 XX New dualPEGylated-leptin bioconjugate useful for treating obesity and
 PT diabetes has polyethylene glycol conjugated to two specific sites on the
 PT leptin molecule.
 XX
 XX Claim 2; Page; 55pp; English.
 XX
 XX The invention relates to a dual-PEGylated leptin bioconjugate comprising
 CC two polyethylene glycol (PEG) moieties attached site-specifically at two
 CC locations in a leptin protein. The invention also provides a site-
 CC directed poly-PEGylation strategy for proteins which results in
 CC homogenous preparations, and can be used with other biologically active
 CC agents including a variety of growth factors and peptide hormones. In
 CC leptin, a serine to cysteine substitution was engineered into the protein
 CC at position 77 (relative to the wild-type mature sequence AAY97871), and
 CC the S77C leptin analogue was PEGylated at the engineered Cys residue and
 CC at the N-terminus. Leptin is a protein which has been shown to cause
 CC weight loss in humans, indicating that it will be useful for causing
 CC weight loss in humans. However, these studies also indicate that leptin
 CC would need to be administered chronically and in a high concentration
 CC formulation to effectively treat obesity in humans. Leptin is insoluble
 CC at physiologic pH at relatively high concentrations, and when injected
 CC into an individual, forms precipitates at the injection site, which
 CC triggers an inflammatory response. The leptin bioconjugate of the
 CC invention provides leptin in a form which allows high dosage without the
 CC problems of leptin precipitates and associated inflammatory response at
 CC the injection site, as seen with prior art leptin compositions. The dual-
 CC PEGylated leptin molecule is large enough to avoid glomerular filtration
 CC and hence kidney vacuolation as seen with a single 20 kDa PEG conjugated
 CC leptin. The dual-PEGylated leptin conjugates are used to effect weight
 CC loss, and may also be used to treat type II diabetes and hyperlipidaemia.

The present sequence is that of mature recombinant human leptin, rHu-Leptin 1-145. This is a natural variant of human leptin 1-146 (see AY95786) in which residue Gln-28 is absent. The invention is directed to glycosylated leptin proteins that have a Stokes' radius greater than that of naturally occurring human leptin. Preferred glycosylated leptins have 1 or more sequence alterations to the present sequence to provide glycosylation sites at amino acid positions 4, 8, 23, 43, 45, 47, 68, 69, 91, 92, 96, 99, 100, 101, 102, 117 and 140, especially 46 + 68, 47 + 68, 68 + 100, 68 + 101, 68 + 102, 68 + 117 and 99 + 101, or 2 + 46 + 68, 23 + 46 + 68, 46 + 68 + 99, 46 + 68 + 101, 47 + 68 + 101, 47 + 68 + 117, 68 + 101 + 117 and 66 + 102 + 117, or 2 + 46 + 68 + 91, 2 + 46 + 68 + 101, 23 + 46 + 68 + 91, 23 + 46 + 68 + 101 and 46 + 68 + 99 + 100, or 2 + 23 + 46 + 68 + 91, 2 + 46 + 68 + 91 + 101 and 23 + 46 + 68 + 91 + 101 (see AY95799-804). Nucleic acids encoding glycosylated leptin are provided.

Pharmaceutical composition for sustained delivery of biologically active agent, comprises biodegradable pH/thermosensitive polymeric matrix containing the biologically active agent.

Disclosure; Page; 51pp; English.

The present invention relates to the use of biodegradable, pH/thermosensitive hydrogels, which can be used to deliver biologically active agents. The present sequence is a mature human leptin protein. Leptin is also known as obesity protein (OB protein). This protein may be used as the biologically active agent for use in the present invention. Note: this sequence is not shown in the specification, but is derived from information given by the inventors about SEQ ID 1 (AAB14265)

Sequence 145 AA;

Query Match	100.0%;	Score 731;	DB 3;	Length 145;
Best Local Similarity	100.0%;	Pred. No. 1.8e-72;		

FT	Misc-difference	74	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	77	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	78	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	89	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	97	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	100	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	102	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	105	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	106	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	107	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	108	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	111	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	112	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	118	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	136	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	138	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	142	"optionally substituted"
FT	FT	/note=	"optionally substituted"
FT	Misc-difference	145	"optionally substituted"
FT	FT	/note=	"optionally substituted"

PN WO9718833-A1.

PD 29-MAY-1997.

AA
PF 04-NOV-1996; 96WO-US017718.

22-NOV-1995: 95US-00561732.

XX
PA (AMGE-) AMGEN INC.XX
PI
pellevmounter MA. Toombs CF:

XX
DR WPI: 1997-310245/28.

Increasing lean tissue content by using obesity protein analogue - for cosmetic use, to improve athletic performance, increase insulin sensitivity, overall body strength and decrease bone resorption.

XX
ps Claim 1: Page: 50pp: English.

AAW34394-W34401 represent mutations and truncations of the mouse and human obesity (OB) proteins shown in AAW22434 and AAW22435. The OB proteins, and these mutations can all be used in the method of the invention. The method of the invention is for increasing lean tissue mass by administration of an OB analogue. The OB proteins are used for cosmetic applications, to improve athletic performance or as adjunct to surgery (e.g. liposuction or implant surgery, cardiac surgery, treatment of broken bones etc.). OB proteins also increase insulin sensitivity and overall body strength, and decrease bone resorption, e.g. for treating diabetes or reducing the amount of insulin needed to treat this disease, or to reverse/improve frailty caused by osteoporosis. Also red blood cell production is increased, increasing mental as well as physical performance. OB are already known to reduce weight but are now found to increase lean mass in non-obese subjects. These OB proteins do not have the side effects associated with use of anabolic steroids, growth hormone etc. Chemical modification of the OB protein (e.g. by attachment to a

CC	water soluble polymer) improves stability, increases circulation time
CC	and/or reduces immunogenicity
XX	
SQ	Sequence 146 AA;

	Query Match	100.0%	Score 731;	DB 2;	Length 146;
	Best Local Similarity	100.0%;	Pred. No. 1.8e-72;		
	Matches 145;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVGTGLDPI	1	PGELHPILTLSKMDQTLAVY	60
Db	2	VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVGTGLDPI	1	PGELHPILTLSKMDQTLAVY	61
Qy	61	QQILTSMPGRNVQIISNDLENLRDLHLVLAFAKSCSLPWPASGL	1	ETLDSLGCVLEASGYST	120
Db	62	QQILTSMPGRNVQIISNDLENLRDLHLVLAFAKSCSLPWPASGL	1	ETLDSLGCVLEASGYST	121

121 EVVALSRLOGSLQDMLWQDLSPGC 145

db 122 EVVAI.SRI.OGSLOPMLWOLDLSPGC 146

RESULT 11

AA97890

ID AAY97890 standard; protein; 146 AA.

AC AAY97890:

DT 29-AUG-2000 (first entry)

XX DE Mutant mature human leptin. methionyl leptin delta-Q28.

XX Leptin analogue; human; polyethylene glycol; site-specific PEGylation;
KW
KW obesity; anorectic; type II diabetes; hyperlipidaemia;
KW antilipoaemic; mutant; mutein.

XX Homo sapiens -

OS	Homo sapiens
OS	Synthetic

XX PN WO200021574-A2.

XX
PD
20-APR-2000XX
PF 13-OCT-1999: 99WO-US024401.

XX
PR 14-OCT-1998: 98US-00172644.

XX (AMGE-) AMGEN INC. PA

XX
PT
Gega C. Kingtler O:XX
DR WPT: 2000-329085/28.

XX New dualPEGylated-leptin bioconjugate useful for treating obesity and
PT diabetes has polyethylene glycol conjugated to two specific sites on the
PT leptin molecule.

XX
PS Claim 2: Page: 55pp: English.

The invention relates to a dual-PEGylated leptin bioconjugate comprising two polyethylene glycol (PEG) moieties attached site-specifically at two locations in a leptin protein. The invention also provides a site-directed poly-PEGylation strategy for proteins which results in homogeneous preparations, and can be used with other biologically active agents including a variety of growth factors and peptide hormones. In leptin, a serine to cysteine substitution was engineered into the protein at position 77 (relative to the wild-type mature sequence, AAY97871), and the S77C leptin analogue was PEGylated at the engineered Cys residue and at the N-terminus. Leptin is a protein which has been shown to cause weight loss in animals, indicating that it will be useful for causing weight loss in humans. However, these studies also indicate that leptin would need to be administered chronically and in a high concentration formulation to effectively treat obesity in humans. Leptin is insoluble

at physiologic pH at relatively high concentrations, and when injected into an individual, forms precipitates at the injection site, which triggers an inflammatory response. The leptin bioconjugate of the invention provides leptin in a form which allows high dosage without the problems of leptin precipitates and associated inflammatory response at the injection site, as seen with prior art leptin compositions. The dual-PEGylated leptin molecule is large enough to avoid glomerular filtration and hence kidney vacuolation as seen with a single 20 kDa PEG conjugated leptin. The dual-PEGylated leptin conjugates are used to effect weight loss, and may also be used to treat type II diabetes and hyperlipidaemia. Sequences AA97889-97893 represent specifically claimed human mature leptin analogues which may be dually-PEGylated according to the invention. Note: The present sequence is not shown in the specification, but is derived from the mature human leptin sequence given on page 12

XX Sequence 146 AA;

Query Match 100.0%; Score 731; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVGLDFIPGLHPILTLKMDQTLAVY 60
DB 2 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVGLDFIPGLHPILTLKMDQTLAVY 61
QY 61 QQLTSMPSRNVQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYST 120
DB 62 QQLTSMPSRNVQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYST 121
QY 121 EVVALSRLOGLQDMLWQLDLSFGC 145
DB 122 EVVALSRLOGLQDMLWQLDLSFGC 146

RESULT 12
AA97262
ID AA97262 standard; protein; 146 AA.

AC AA97262;
XX 10-AUG-2000 (first entry)
DT Mature recombinant methionyl human leptin, rHu-leptin 1-145.
DE rHu-leptin 1-145; recombinant; mature protein; human leptin;
KW predisposition; screening; obesity.
XX Homo sapiens.

Key Location/Qualifiers
FT Protein 2..145
FT /label= mature_protein

XX WO200020872-A1.

XX 13-APR-2000.

XX 21-SEP-1999; 99WO-US021903.

XX 02-OCT-1998; 98US-00165453.

XX 27-OCT-1998; 98US-00181836.

XX (AMGE-) AMGEN INC.

XX Mccamish MA, Hunt P, Lubina JA;

XX WPI; 2000-339110/29.

XX Novel method for determining a predisposition to successful leptin

XX treatment of obesity by measuring baseline serum leptin levels.

XX Disclosure; Page; 40pp; English.

XX

CC This is the mature, recombinant methionyl human leptin, designated rHu-
CC Leptin 1-145, which is a variant of rHu-Leptin 1-146 (see AA97262). When
CC compared with rHu-Leptin 1-146, this sequence has a glutamine absent at
CC position 28. The claimed method for determining the predisposition of an
CC obese individual to respond to leptin, leptin analog or derivative
CC treatment comprises determining a leptin level in the individual prior to
CC treatment, and ascertaining if the leptin level is in the bottom 25 or 33
CC percent of leptin levels of obese individuals. The rHu-Leptin 1-146 or 1-
CC 145 (see AA97262) or other analogues (e.g. AA97263-66) may be used in
CC treatment. The method can be used as a screening tool to determine the
CC likelihood that an obese individual (i.e. an individual with a body mass
CC index of greater than 27) not having co-morbidities of obesity, such as
CC diabetes, dislipidaemias and hypertension, will respond to leptin
CC administration with weight loss. Leptin is used for weight modulation
CC (especially weight reduction), treatment of diabetes, blood lipid
CC reduction, increasing lean body mass, and increasing insulin sensitivity,
CC as well as the treatment of conditions associated with fertility, wound
CC healing, hematopoietic conditions, angiogenic conditions and chronic
CC stress conditions. Prescreening an individual's predisposition to respond
CC to leptin administration may save on unnecessary treatments. Note: The
CC specification provides the sequence of the mature protein which appears
CC on pages 12-13, a methionyl residue is added at position 1 to create
CC this rHu-Leptin 1-145 as described in the specification
XX Sequence 146 AA;

Query Match 100.0%; Score 731; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVGLDFIPGLHPILTLKMDQTLAVY 60
DB 2 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVGLDFIPGLHPILTLKMDQTLAVY 61
QY 61 QQLTSMPSRNVQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYST 120
DB 62 QQLTSMPSRNVQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYST 121
QY 121 EVVALSRLOGLQDMLWQLDLSFGC 145
DB 122 EVVALSRLOGLQDMLWQLDLSFGC 146

RESULT 13
AAW00537
ID AAW00537 standard; protein; 165 AA.

XX AAW00537;

XX 13-SEP-1996 (first entry)

XX Human obesity protein variant #15.

XX Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
XX food intake; energy expenditure; high blood pressure; cholesterol; human;
XX gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.

XX Synthetic.

Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
FT Misc-difference 18
FT /note= "y18G mutation"
FT Misc-difference 19
FT /note= "V19S mutation"
FT Misc-difference 20
FT /note= "Q20P mutation"
FT Misc-difference 21
FT /note= "delta A21 mutation"
FT Protein 22..165
FT /note= "obesity protein"

XX

PN GB2292382-A.
 XX 21-FEB-1996.
 XX 17-AUG-1995; 95GB-00016947.
 XX 17-AUG-1994; 94US-00292345.
 PR 30-NOV-1994; 94US-00347563.
 PR 10-MAY-1995; 95US-00438431.
 PR 07-JUN-1995; 95US-00483211.
 XX (UTRQ) UNIV ROCKEFELLER.
 XX Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;
 PI Burley SK;
 XX WPT; 1996-099009/11.
 DR Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
 PT reducing wt. in treatment of diabetes, high blood pressure and high
 PT cholesterol and for cosmetic reasons.
 XX Claim 12; Page ?; 304pp; English.
 XX AAR92725-R92730, and AAW00516-W00537 represent variants of the murine and
 CC human obesity polypeptides (OBP). This sequence has residues 18-21
 CC mutated in comparison to the wild type sequences (represented by AAR92719
 CC and AAR92720). OBP (also known as leptin) is a hormone involved in the
 CC regulation of body weight. This sequence has effects on both food intake
 CC and energy expenditure. OBP and its analogues are useful for modifying
 CC body weight (optionally combined with known medicaments), for treating
 CC diabetes, high blood pressure or high cholesterol. The DNA encoding this
 CC sequence (and sequences complementary to it) can be used in gene therapy
 CC for modifying body weight. This protein can be used for reducing weight
 CC for health or cosmetic reasons in obese humans, or to produce leaner food
 CC animals. Antagonists of OBP (including antibodies) are useful for
 CC increasing body weight, e.g. for treating weight loss associated with
 CC cancer, or for cosmetic reasons in humans, or for production of Kobe beef
 CC or Foie gras in domestic animals. OBP antibodies (Ab) can also be used in
 CC diagnostic immunoassays for the presence of OBP. The formation of Ab-OBP
 CC complexes enables in vitro evaluation of levels of OBP in a sample,
 CC especially to detect diseases associated with elevated or decreased
 CC levels, and to monitor treatment of these diseases
 XX Sequence 165 AA;
 SQ Query Match 100.0%; Score 731; DB 2; Length 165;
 Best Local Similarity 100.0%; Pred. No. 2.le-72;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPIQKVDTKTLIKTIVTRINDISHTSVSKQKVTGLDFIPGLHPILTLKMDOTLAVY 60
 DB 21 VPIQKVDTKTLIKTIVTRINDISHTSVSKQKVTGLDFIPGLHPILTLKMDOTLAVY 80
 QY 61 QQILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYST 120
 DB 81 QQILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYST 140
 QY 121 EVVALSRQGLQDMWLQDLSPGC 145
 DB 141 EVVALSRQGLQDMWLQDLSPGC 165
 RESULT 14
 ID AAW00515
 XX AAW00515 standard; protein; 166 AA.
 XX AAW00515;
 XX 12-SEP-1996 (first entry)
 DT Human obesity protein variant.
 XX

KW Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
 KW food intake; energy expenditure; high blood pressure; cholesterol; human;
 KW gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /note= "signal peptide"
 FT Protein 22..166
 FT /note= "obesity protein"
 XX GB2292382-A.
 XX 21-FEB-1996.
 XX 17-AUG-1995; 95GB-00016947.
 XX 17-AUG-1994; 94US-00292345.
 PR 30-NOV-1994; 94US-00347563.
 PR 10-MAY-1995; 95US-00438431.
 PR 07-JUN-1995; 95US-00483211.
 XX (UTRQ) UNIV ROCKEFELLER.
 XX Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;
 PI Burley SK;
 XX WPT; 1996-099009/11.
 DR Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
 PT reducing wt. in treatment of diabetes, high blood pressure and high
 PT cholesterol and for cosmetic reasons.
 XX Claim 2; Page 174; 304pp; English.
 XX AAW00514 and AAW00515 represent variants of the murine and human obesity
 CC polypeptides (OBP), respectively. These sequences lack the Gln residue
 CC located at position 49 of the wild type sequences (represented by
 CC AAR92719 and AAR92720 respectively). OBP (also known as leptin) is a
 CC hormone involved in the regulation of body weight. This sequence has
 CC effects on both food intake and energy expenditure. OBP and its analogues
 CC are useful for modifying body weight (optionally combined with known
 CC medicaments), for treating diabetes, high blood pressure or high
 CC cholesterol. The DNA encoding this sequence (and sequences complementary
 CC to it) can be used in gene therapy for modifying body weight. This
 CC protein can be used for reducing weight for health or cosmetic reasons in
 CC obese humans, or to produce leaner food animals. Antagonists of OBP
 CC (including antibodies) are useful for increasing body weight, e.g. for
 CC treating weight loss associated with cancer, or for cosmetic reasons in
 CC humans, or for production of Kobe beef or Foie gras in domestic animals.
 CC OBP antibodies (Ab) can also be used in diagnostic immunoassays for the
 CC presence of OBP. The formation of Ab-OBP complexes enables in vitro
 CC evaluation of levels of OBP in a sample, especially to detect diseases
 CC associated with elevated or decreased levels, and to monitor treatment of
 CC these diseases
 XX Sequence 166 AA;
 SQ Query Match 100.0%; Score 731; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2.le-72;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPIQKVDTKTLIKTIVTRINDISHTSVSKQKVTGLDFIPGLHPILTLKMDOTLAVY 60
 DB 22 VPIQKVDTKTLIKTIVTRINDISHTSVSKQKVTGLDFIPGLHPILTLKMDOTLAVY 81
 QY 61 QQILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYST 120
 DB 82 QQILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYST 141
 QY 121 EVVALSRQGLQDMWLQDLSPGC 145

Db 142 EVVALSRQSLQDMLWQLDLSPGC 166

RESULT 15

AAW00525
ID AAW00525 standard; protein; 166 AA.

XX AC AAW00525;

XX DT 13-SEP-1996 (first entry)

XX DE Human obesity protein variant #5.

XX KW Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
KW food intake; energy expenditure; high blood pressure; cholesterol; human;
KW gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.

XX OS Synthetic.

XX PH Key Location/Qualifiers
FT Peptide 1..21 /note= "signal peptide"
FT Misc-difference 2 /note= "H2G mutation"
FT Misc-difference 3 /note= "W3S mutation"
FT Misc-difference 4 /note= "G4S mutation"
FT Misc-difference 5 /note= "TSH mutation"
FT Misc-difference 6 /note= "L6H mutation"
FT Misc-difference 7 /note= "C7H mutation"
FT Misc-difference 8 /note= "G8H mutation"
FT Misc-difference 9 /note= "F9H mutation"
FT Misc-difference 10 /note= "L10H mutation"
FT Misc-difference 11 /note= "W11S mutation"
FT Misc-difference 12 /note= "L12S mutation"
FT Misc-difference 13 /note= "W13G mutation"
FT Misc-difference 14 /note= "P14L mutation"
FT Misc-difference 15 /note= "Y15V mutation"
FT Misc-difference 16 /note= "L16P mutation"
FT Misc-difference 17 /note= "F17R mutation"
FT Misc-difference 18 /note= "Y18G mutation"
FT Misc-difference 19 /note= "V19S mutation"
FT Misc-difference 20 /note= "Q20H mutation"
FT Misc-difference 21 /note= "A21M mutation"
FT Protein 22..166 /note= "obesity protein"

XX GB2292382-A.

XX PD 21-FEB-1996.

XX PF 17-AUG-1995; 95GB-00016947.

XX PR 17-AUG-1994; 94US-00292345.

XX PR 30-NOV-1994; 94US-00347563.

PR 10-MAY-1995; 95US-00438431.
PR 07-JUN-1995; 95US-00483211.
XX
XX PA (UYRQ) UNIV ROCKEFELLER.
XX
XX PI Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;
XX PI Burley SK;
XX DR WPI; 1996-099009/11.

XX OB Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
FT reducing wt. in treatment of diabetes, high blood pressure and high
FT cholesterol and for cosmetic reasons.

XX PS Claim 11; Page ?; 304pp; English.

XX CC AAR92725-R92730, and AAW00516-W00537 represent variants of the murine and
CC human obesity polypeptides (OBP). This sequence has the signal peptide
CC region (residues 1-21) mutated in comparison to the wild type sequences
CC (represented by AAR92719 and AAR92720). OBP (also known as leptin) is a
CC hormone involved in the regulation of body weight. This sequence has
CC effects on both food intake and energy expenditure. OBP and its analogues
CC are useful for modifying body weight (optionally combined with known
CC medicaments), for treating diabetes, high blood pressure or high
CC cholesterol. The DNA encoding this sequence (and sequences complementary
CC to it) can be used in gene therapy for modifying body weight. This
CC protein can be used for reducing weight for health or cosmetic reasons in
CC obese humans, or to produce leaner food animals. Antagonists of OBP
CC (including antibodies) are useful for increasing body weight, e.g. for
CC treating weight loss associated with cancer, or for cosmetic reasons in
CC humans, or for production of Kobe beef or Foie gras in domestic animals.
CC OBP antibodies (Ab) can also be used in diagnostic immunoassays for the
CC presence of OBP. The formation of Ab-OBP complexes enables in vitro
CC evaluation of levels of OBP in a sample, especially to detect diseases
CC associated with elevated or decreased levels, and to monitor treatment of
CC these diseases

XX SQ Sequence 166 AA;

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.1e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVGTGLDFIPGLHPILTLKMDQTLAVY 60

Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVGTGLDFIPGLHPILTLKMDQTLAVY 81

Qy 61 QQILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYST 120

Db 82 QQILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYST 141

Qy 121 EVVALSRQSLQDMLWQLDLSPGC 145

Db 142 EVVALSRQSLQDMLWQLDLSPGC 166

Search completed: May 4, 2006, 21:52:16
Job time : 139.526 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:50:51 ; Search time 27.4055 Seconds
(without alignments)
509.074 Million cell updates/sec

Title: US-10-623-189-2
Perfect score: 731
Sequence: 1 VPIQKQVDDTKTLIKTIVTR.....SRLLQSLQDMLQDLSPGC 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	731	100.0	166	2	I53166
2	720.5	98.6	167	1	LTHU
3	603.5	82.6	167	1	LTHU
4	589.5	80.6	167	1	LTHU
5	589.5	80.6	167	2	I55622
6	83	11.4	1600	2	A83281
7	82.5	11.3	790	2	H71509
8	81.5	11.1	829	2	T01362
9	79	10.8	922	2	H84583
10	78	10.7	420	2	S75514
11	78	10.7	674	2	S46092
12	77.5	10.6	186	2	G82638
13	77.5	10.6	574	1	B42374
14	77.5	10.6	821	2	A81126
15	77	10.5	444	2	S54039
16	77	10.5	1228	2	S46754
17	76.5	10.5	362	2	A83967
18	76.5	10.5	822	2	E86305
19	75.5	10.3	639	2	A20055
20	75	10.3	823	2	H72282
21	75	10.3	1191	2	S76414
22	75	10.3	1438	2	S59792
23	74	10.1	403	2	T26551
24	73.5	10.1	177	2	A38106
25	73.5	10.1	296	2	D70424
26	73.5	10.1	296	2	D88511
27	73.5	10.1	348	2	A22477
28	73.5	10.1	521	1	A44267
29	73.5	10.1	696	2	S44912

ALIGNMENTS

RESULT 1

I53166
leptin precursor - human
N;Alternate names: obese
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: I53166; G02328
R;Masuzaki, H.; Ogawa, Y.; Isse, N.; Satoh, N.; Okazaki, T.; Shigemoto, M.; Mori, K.;
Diabetes 44, 855-858, 1995
A;Title: Human obese gene expression. Adipocyte-specific expression and regional differ
A;Reference number: I53166; MUID:95309556; PMID:7789654
A;Accession: I53166
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-166 <RES>
A;Cross-references: UNIPROT:P41159; UNIPARC:UPI000014DL64; GB:D49487; NID:g904211; PID:
R;Chehab, F.F.; Lim, M.E.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01063
A;Accession: G02328
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-166 <CHE>
A;Cross-references: UNIPARC:UPI000014DL64; EMBL:U43415; NID:g1163105; PIDN:AAC31660.1;
C;Genetics:
A;Gene: GDB:LEP; OB; OBS
A;Cross-references: GDB:136420; OMIM:164160
A;Map position: 7q32.1-7q32.1
A;Introns: 48/3
C;Superfamily: leptin

Query Match 100.0%; Score 731; DB 2; Length 166;

Best Local Similarity 100.0%; Pred. No. 2.2e-59; Mismatches 0; Indels 0; Gaps 0;

Matches 145; Conservative 0;

QY 1 VPIQKQVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFPGLHPILTLKMDQTLAVY 60

DB 22 VPIQKQVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFPGLHPILTLKMDQTLAVY 81

QY 61 QQILTSPSRNVIQISNDLENLRDLHLVAFPSKSHLPWASGLETSLGGLVLEASGYST 120

DB 82 QQILTSPSRNVIQISNDLENLRDLHLVAFPSKSHLPWASGLETSLGGLVLEASGYST 141

QY 121 EWALSRLLQSLQDMLQDLSPGC 145

DB 142 EWALSRLLQSLQDMLQDLSPGC 166

RESULT 2

LTHU

leptin precursor - human

N;Alternate names: obese protein; obesity factor

C;Species: Homo sapiens (man)
C;Date: 28-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: A38952; JEO148
R;Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A;Title: Positional cloning of the mouse obese gene and its human homologue.
A;Reference number: S50863; MUID:95075453; PMID:7984236
A;Accession: A38952
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-167 <ZHA>
A;Cross-references: UNIPROT:P41159; UNIPARC:UPI00000308D4; GB:U18915; NID:G623331; PIDN:
R;Liao, H.J.; Deng, Y.B.; Chen, X.M.; Ye, Y.Z.
Chinese Biochem. J. 13, 249-253, 1997
A;Title: Cloning of Chinese obesity gene and construction of prokaryotic expression vec
A;Reference number: JEO148
A;Accession: JEO148
A;Molecule type: mRNA
A;Residues: 'M', 22-167 <LIA>
A;Cross-references: UNIPARC:UPI0000158347
A;Experimental source: adipose
A;Note: the author translated GAC for residue 148 as Ser
C;Genetics:
A;Gene: GDB:LEP; OB; OBS
A;Cross-references: GDB:136420; OMIM:164160
A;Map position: 7q31.3-q31.3
C;Superfamily: leptin
C;Keywords: adipose tissue
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-167/Product: leptin #status predicted <MAT>

Query Match 98.6%; Score 720.5; DB 1; Length 167;
Best Local Similarity 99.3%; Pred. No. 2e-58; Mismatches 0; Indels 1; Gaps 1;
Matches 145; Conservative 0

QY 1 VPIQKVDDTKTIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
DB 22 VPIQKVDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 60 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 119
DB 82 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 141

QY 120 TEVALSRLOQSLQDMLWQDLSPGC 145
DB 142 TEVALSRLOQSLQDMLWQDLSPGC 167

RESULT 3
LTPS
leptin precursor - mouse
N;Alternate names: obese protein
C;Species: Mus musculus (house mouse)
C;Date: 14-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: S50863
R;Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A;Title: Positional cloning of the mouse obese gene and its human homologue.
A;Reference number: S50863; MUID:95075453; PMID:7984236
A;Accession: S50863
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-167 <ZHA>
A;Cross-references: UNIPROT:P41160; UNIPARC:UPI00000308D4; EMBL:U18812; NID:G746416; PIDN:
C;Superfamily: leptin
C;Keywords: adipose tissue
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-167/Product: leptin #status predicted <MAT>

Query Match 82.6%; Score 603.5; DB 1; Length 167;
Best Local Similarity 84.2%; Pred. No. 9e-48; Mismatches 9; Indels 1; Gaps 1;
Matches 123; Conservative 13

QY 1 VPIQKVDDTKTIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
DB 22 VPIQKVDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 60 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 119
DB 82 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 141

QY 120 TEVALSRLOQSLQDMLWQDLSPGC 145
DB 142 TEVALSRLOQSLQDMLWQDLSPGC 167

RESULT 4

LTPS

leptin precursor - rat
N;Alternate names: obese protein; obesity factor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: PC4034; JC4142
R;Funahashi, T.; Shimomura, I.; Hiraoka, H.; Arai, T.; Takahashi, M.; Nakamura, T.; Noz
Biochem. Biophys. Res. Commun. 211, 469-475, 1995
A;Title: Enhanced expression of rat obese (ob) gene in adipose tissues of ventromedial
A;Reference number: PC4034; MUID:95314614; PMID:7794258
A;Accession: PC4034
A;Molecule type: mRNA
A;Residues: 1-167 <FUN>
A;Cross-references: UNIPROT:P50596; UNIPARC:UPI0000038DAF
A;Experimental source: adipose tissue
A;Note: The authors translated the codon AAA for residue 32 as Thr
R;Murakami, T.; Shima, K.
Biochem. Biophys. Res. Commun. 209, 944-952, 1995
A;Title: Cloning of rat obese cDNA and its expression in obese rats.
A;Reference number: JC4142; MUID:95251725; PMID:7733988
A;Accession: JC4142
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-167 <MUR>
A;Cross-references: UNIPARC:UPI0000038DAF; DDBJ:D49653; NID:G995614; PIDN:BAA08529.1; P
A;Experimental source: liver
C;Comment: This protein is proposed to function as part of a signalling pathway from ad
C;Genetics:
A;Gene: obese
C;Superfamily: leptin
C;Keywords: adipose tissue
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-167/Product: leptin #status predicted <MAT>

Query Match 80.6%; Score 589.5; DB 1; Length 167;
Best Local Similarity 82.9%; Pred. No. 1.7e-46; Mismatches 13; Indels 1; Gaps 1;
Matches 121; Conservative 13

QY 1 VPIQKVDDTKTIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
DB 22 VPIQKVDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 60 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 119
DB 82 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSIGGVLEASGYS 141

QY 120 TEVALSRLOQSLQDMLWQDLSPGC 145
DB 142 TEVALSRLOQSLQDMLWQDLSPGC 167

RESULT 5

rat ob - rat

I55622
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I55622
R;Ogawa, Y.; Maizaki, H.; Isse, N.; Okazaki, T.; Mori, K.; Shigemoto, M.; Satoh, N.; T
J. Clin. Invest. 96, 1647-1652, 1995

A;Title: Molecular cloning of rat obese cDNA and augmented gene expression in genetically
A;Reference number: I55622; MUID:95386724; PMID:7657834
A;Accession: I55622
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-167 <RES>
A;Cross-references: UNIPARC:UPI0000038DAF; GB:D45862; NID:g1018990; PIDN:BAA08296.1; PID
C;Superfamily: leptin

Query Match 80.6%; Score 589.5; DB 2; Length 167;
Best Local Similarity 82.9%; Pred. No. 1.7e-46;
Matches 121; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

Qy 1 VPIQVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTSKMDQTLAV 59

Db 22 VPIHKVQDDTKTLIKTIVTRINDISHTQSVSQRQVGTGLDFIPGLHPILTSKMDQTLAV 81

Qy 60 YQILTSMPNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS 119

Db 82 YQILTSMPNRNVQISNDLENRLDLHLVAFSKSCHLPQTRGLQKRPESLDGVLEASLYS 141

Qy 120 TEVVALSRLOGSLQDMLWQDLSPGC 145

Db 142 TEVVALSRLOGSLQDILQQLDLSPEC 167

RESULT 6

AB3281 glutamate dehydrogenase (EC 1.4.1.2) [imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 05-Oct-2004

C;Accession: AB3281

R;DelVecchio, V.G.; Kaprat, R.J.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

M.; Mazur, M.; Gotsman, E.; Seikov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens

A;Reference number: AD3252; PMID:11756688

C;Accession: AB3281

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1600 <CUR>

A;Cross-references: UNIPROT:Q8YJ55; UNIPARC:UPI0000057BD4; GB:AE008917; PIDN:AAL51413.1;

A;Superfamily: glutamate dehydrogenase, M14104 type

C;Genetics:

A;Gene: BMEI0231

A;Map position: 1

C;Superfamily: glutamate dehydrogenase, M14104 type

C;Keywords: oxidoreductase

Query Match 11.4%; Score 83; DB 2; Length 1600;

Best Local Similarity 25.6%; Pred. No. 38;

Matches 33; Conservative 22; Mismatches 52; Indels 22; Gaps 5;

Qy 6 VQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTSKMDQTLAVYQILTL 65

Db 97 VNDNMPFLDSIMGELND-HTS-----QIFMVVHPVLDSREKDBELVILGEASQ 144

Qy 66 SMPNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYSTEVVAL 125

Db 145 LAPAKGVRS-----LVQIHPALSKQAKADTAGLKR--LGQV--RGAIVSDWKPMPL 194

Qy 126 SRLQSLQD 134

Db 195 KRLDGAIDD 203

RESULT 7

H71509

phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Chlamydia trachomatis (serotype D,

C;Species: Chlamydia trachomatis

C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C;Accession: H71509

R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra

A;Reference number: A71570; MUID:99000809; PMID:9784136

A;Accession: H71509

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-790 <ARN>

A;Cross-references: UNIPROT:O84481; UNIPARC:UPI0000136445; GB:AE001321; GB:AE001273; NI

A;Experimental source: serotype D, strain UW-3/Cx

C;Genetics:

A;Gene: pheT

C;Superfamily: phenylalanine-tRNA ligase beta chain

C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 11.3%; Score 82.5; DB 2; Length 790;

Best Local Similarity 27.5%; Pred. No. 17;

Matches 46; Conservative 26; Mismatches 54; Indels 41; Gaps 10;

Qy 2 PIQKVQDDTKTLI-----KTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTSKMDQ 55

Db 395 PIQKIGDDSPSLSVRPKTI-KRLDIELSTAEIVAKLSSLSGF-----Q 439

Qy 56 TLAVYQQILTSMPS--RNVIQISNDLENRLDLHLVAFSKSCH--LPWASGLETLD----- 107

Db 440 TAVEEQAVRVEVPSYRHDIQEETDL--VEICRTTFFVQKTKILPTTPIYSLKRELT 497

Qy 108 --SLGGVLEASGYS---TEVVALSRLOGSL---QDMLWQL--DLSPG 144

Db 498 FLANGGLQQFTTYSLLDTEVSSLSLQESSLIPVQNSSWKLRLDLSLPG 544

RESULT 8

T01362

probable myosin heavy chain At2g34730 - Arabidopsis thaliana

N;Alternate names: hypothetical protein T29F13.6

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Accession: T01362; C84760

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kan

submitted to the EMBL Data Library, May 1998

A;Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.

A;Reference number: 214179

A;Accession: T01362

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-829 <ROU>

A;Cross-references: UNIPROT:O64584; UNIPARC:UPI000004A13E; EMBL:AC003096; NID:g3132469;

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: C84760

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-829 <STO>

A;Cross-references: UNIPARC:UPI000004A13E; GB:AE002093; NID:g3132472; PIDN:AAC16261.1;

C;Genetics:

A;Gene: At2g34730; T29F13.6

A;Map position: 2

A;Introns: 728/2; 770/3

Query Match 11.1%; Score 81.5; DB 2; Length 829;

Best Local Similarity 21.0%; Pred. No. 23;

Matches 33; Conservative 27; Mismatches 46; Indels 51; Gaps 5;

Qy 3 IQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTSKMDQTLAVY-- 60

Db 57 ISRVVSD--SIIRGVWTAIESDAEAKIAQK-----LELSKIRETLVYH 100

Qy 61 -----QQILTSMPSNRVQISNDLENRLDLHLVAFSKSCHLPW 99

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:47:48 ; Search time 144.502 Seconds
(without alignments)
707.961 Million cell updates/sec

Title: US-10-623-189-2

Perfect score: 731

Sequence: 1 VPIQVQDDTKLIKTIIVTR.....SRLQGSIQDMLWLQDLSPGC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720.5	98.6	167	1	P41159 homo sapien
2	720.5	98.6	167	1	O6NT58 HUMAN
3	717.5	98.2	146	1	OB_PANTR
4	712.5	97.5	146	1	OB_GORGO
5	705.5	96.5	146	1	OB_PONPY
6	656.5	89.8	167	1	OB_MACMU
7	623.5	85.3	167	1	OB_FELCA
8	612.5	83.8	146	2	O6T8R8 BUBBU
9	612.5	83.8	167	1	OB_BOVIN
10	612.5	83.8	167	1	OB_BUBBU
11	611.5	83.7	167	1	OB_PIG
12	611.5	83.7	167	2	O5TIL9 PTG
13	608.5	83.2	146	1	OB_SHEEP
14	608.5	83.2	167	2	O5EAE4 BOVIN
15	603.5	82.6	146	2	O4VW71_CTEID
16	603.5	82.6	167	1	OB_MOUSE
17	603.5	82.6	167	2	O544U0 MOUSE
18	599.5	82.0	146	2	O4VW70_HYPMO
19	599.5	82.0	146	2	O4VW72 CARAU
20	599.5	82.0	146	2	O4LLM8_CYPCA
21	597	81.7	163	1	OB_CHICK
22	596.5	81.6	146	2	O4VM67 MEGAM
23	593.5	81.2	146	2	O4VM68_SILAS
24	589.5	80.6	167	1	OB_RAT
25	588.5	80.5	146	2	O4VM66_9PERC
26	588.5	80.5	146	2	O4VM81_9TELE
27	588	80.4	147	2	O4VM60_ANAPL
28	587	80.3	145	1	OB_MEIGA
29	581.5	79.5	146	2	O4VM69_ARINO
30	580.5	79.4	167	1	OB_CANFA
31	507	69.4	145	1	OB_HORSE

32	495.5	67.8	167	1	OB_SMICR
33	493	67.4	119	2	O861R2_BUBBU
34	483.5	66.1	118	2	O4VYB6_9RODE
35	477	65.3	118	2	O8MK60_ALOLA
36	476	65.1	118	2	O8MK58_VULVU
37	474	64.8	118	2	O8MK59_NYCPR
38	469	64.2	118	2	O8MK61_CANFA
39	457	62.5	110	2	O56QP8_SHEEP
40	450.5	61.6	123	2	O95KW9_MYOLU
41	449.5	61.5	167	1	OB_HALGR
42	447.5	61.2	167	1	OB_PHOVI
43	444	60.7	109	2	O866S7_BUBBU
44	434	59.4	109	2	O864V1_CAMDR
45	387	52.9	106	2	O95MG5_CAPHI

ALIGNMENTS

RESULT 1
OB_HUMAN STANDARD; PRT; 167 AA.
AC P41159; O15158; Q56A88;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-FEB-2005 (Rel. 48, Last annotation update)
DE Leptin precursor (Obesity factor) (Obese protein).
GN Name=LEP; Synonyms=OB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=95075453; PubMed=7984236; DOI=10.1038/372425a0;
RA Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RT "Positional cloning of the mouse obese gene and its human homologue.";
RL Nature 372:425-432(1994).
RN [2]
RP ERRATUM.
RA Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
RL Nature 374:479-479(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95309556; PubMed=7789654;
RA Masuzaki H., Ogawa Y., Isse N., Satoh N., Okazaki T., Shigemoto M.,
RA Mori K., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,
RA Nakao K.;
RT "Human obese gene expression. Adipocyte-specific expression and regional differences in the adipose tissue.";
RL Diabetes 44:855-858(1995).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96223958; PubMed=8626726; DOI=10.1074/jbc.271.8.3971;
RA Gong D.W., Bi S., Pratley R.E., Weintraub B.D.;
RT "Genomic structure and promoter analysis of the human obese gene.";
RL J. Biol. Chem. 271:3971-3974(1996).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96070903; PubMed=7499240; DOI=10.1074/jbc.270.46.27728;
RA Isse N., Ogawa Y., Tamura N., Masuzaki H., Mori K., Okazaki T.,
RA Satoh N., Shigemoto M., Yoshimasa Y., Nishi S., Hosoda K., Inazawa J.,
RA Nakao K.;
RT "Structural organization and chromosomal assignment of the human obese gene.";
RL J. Biol. Chem. 270:27728-27733(1995).
RN [7]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=96198511; PubMed=8621021;
 RA Niki T., Mori H., Tamori Y., Kiehimoto-Haehiramoto M., Ueno H.,
 RA Araki S., Maugi J., Sawant N., Majithia H.R., Rais N.,
 RA Hashiramoto M., Taniguchi H., Kasuga M.;
 RT "Human obese gene: molecular screening in Japanese and Asian Indian
 RT NIDDM patients associated with obesity.";
 RL Diabetes 45:675-678(1996).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Lu L., Fu Z., Xu M., Fu Y., Hu Z.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT MET-94.
 RA Bieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Bertucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
 RT "SeattlesNP8. NHLBI Hu66682 program for genomic applications, UW-
 RT FRCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Placenta;
 RX STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP INTERACTION WITH SIGLEC6.
 RX MEDLINE=99357812; PubMed=10428856; DOI=10.1074/jbc.274.32.22729;
 RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
 RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
 RA Varki A., Kastelein R.A.;
 RT "OB-BP1/Siglec-6. A leptin- and sialic acid-binding protein of the
 RT immunoglobulin superfamily.";
 RL J. Biol. Chem. 274:22729-22738(1999).
 RN [12]
 RP ERRATUM.
 RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
 RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
 RA Varki A., Kastelein R.A.;
 RL J. Biol. Chem. 274:28058-28058(1999).
 RN [13]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97309492; PubMed=9166907; DOI=10.1016/S0014-5793(97)00353-0;
 RA Kline A.D., Becker G.W., Churgay L.M., Landen B.E., Martin D.K.,
 RA Muth W.L., Rathnachalam R., Richardson J.M., Schoner B., Ulmer M.,
 RA Hale J.E.;
 RT "Leptin is a four-helix bundle: secondary structure by NMR.";
 RL FEBS Lett. 407:239-242(1997).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ÅNGSTRÖMS).
 RX MEDLINE=97289390; PubMed=9144295;
 RA Zhang F., Basinski M.B., Beals J.M., Briggs S.L., Churgay L.M.,
 RA Clawson D.K., Dimarichi R.D., Furman T.C., Hale J.E., Heiling H.M.,
 RA Schoner B.E., Smith D.P., Zhang X.Y., Wery J.P., Schevitz R.W.;
 RT "Crystal structure of the obese protein leptin-E100.";
 RL Nature 387:206-209(1997).

RN [15]
 RP VARIANT MET-94.
 RA Bartholomew D.W., McClellan J.M.;
 RT "A novel polymorphism in the leptin gene.";
 RL Hum. Mutat. 12:220-220(1998).
 RN [16]
 RP VARIANT MORBID OBESITY TRP-105.
 RX MEDLINE=98160176; PubMed=9500540;
 RA Strobel A., Issad T., Camoin L., Ozata M., Strosberg A.D.;
 RT "A leptin missense mutation associated with hypogonadism and morbid
 RT obesity.";
 RL Nat. Genet. 18:213-215(1998).
 CC -I- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass.
 CC -I- SUBUNIT: Interacts with SIGLEC6.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- DISEASE: Defects in LEP may be a cause of autosomal recessive
 CC obesity [MIM:601665].
 CC -I- SIMILARITY: Belongs to the leptin family.
 CC -I- DATABASE: NAME=Ref Systems' cytokine mini-reviews: LEP;
 CC WWW="http://www.rndsystems.com/asp/q sitebuilder.asp?bodyid=213".
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; U18915; AAA60470.1; --; mRNA.
 DR EMBL; D49487; BAA08448.1; --; mRNA.
 DR EMBL; U43653; AAC50400.1; --; mRNA.
 DR EMBL; U43415; AAC31660.1; --; Genomic DNA.
 DR EMBL; D63710; BAA09839.1; --; Genomic DNA.
 DR EMBL; D63519; BAA09787.1; --; Genomic DNA.
 DR EMBL; AF008123; AAB63507.1; --; mRNA.
 DR EMBL; AJ996373; AAX81413.1; --; Genomic DNA.
 DR EMBL; BC060830; AAH60830.1; --; mRNA.
 DR EMBL; BC069452; AAH69452.1; --; mRNA.
 DR EMBL; BC069527; AAH69527.1; --; mRNA.
 DR PIR; A38952; LTHU
 DR PIR; I53166; I53166.
 DR PDB; IAX8; X-ray; @=22-167.
 DR Ensembl; ENSG0000174697; Homo sapiens.
 DR HGNC; HGNC:6553; LEP.
 DR MIM; 164160; --
 DR MIM; 601665; --
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0006112; P:energy reserve metabolism; TAS.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000065; Leptin.
 DR PANTHER; PTHR11724; Leptin; 1.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PD0495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 DR 3D-structure; Diabetes mellitus; Disease mutation; Obesity;
 KW Polymorphism; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167
 FT VARIANT 49 49
 FT VARIAT 94 94 Missing (in 30% the clones).
 FT VARIAT 105 105 V -> M (in dbSNP:17151919).
 FT VARIAT 105 105 /FTID=VAR 004197.
 FT VARIAT 105 105 R -> W (in morbid obesity and
 FT VARIAT 105 105 hypogonadism).
 FT VARIAT 110 110 /FTID=VAR 008094.
 FT VARIAT 110 110 V -> M (in dbSNP:1800564).
 FT CONFLICT 96 96 /FTID=VAR 011955.
 FT HELIX 25 44 Q -> R (in Ref. 8).

DR ProDom; PD005698; Leptin; 1.
 KW Obesity. 96 146 By similarity.
 FT DISULFID 146 AA; 16059 MW; 02C42A06B554D55C CRC64;
 -SQ SEQUENCE 146 AA; 16059 MW; 02C42A06B554D55C CRC64;
 Query Match 98.2%; Score 717.5; DB 1; Length 146;
 Best Local Similarity 98.6%; Pred. No. 3.4e-58;
 Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 59
 DB 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSQKVTGLDFIPGLHPILTLKMDQTLAV 60
 QY 60 YQILTSMPSRNVQISNDLENRLDLHLAFSKSCHLPWASGLETLDSIGGVLEASGYS 119
 DB 61 YQILTSMPSRNVQISNDLENRLDLHLAFSKSCHLPWASGLETLDSIGGVLEASGYS 120
 QY 120 TEVVALSRQSGSLQDMLWQLDLSGPC 145
 DB 121 TEVVALSRQSGSLQDMLWQLDLSGPC 146
 RESULT 4
 OB_GORGO OB_GORGO STANDARD; PRT; 146 AA.
 ID OB_GORGO
 AC Q95189;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leptin (Obesity factor).
 GN Names=LEP; Synonyms=OB;
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Gorilla.
 OX NCBI_TaxID=9595;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Smith D.P., Zhang X., Hsiung H.M.;
 RT "Gorilla leptin genomic sequence."
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- SIMILARITY: Belongs to the leptin family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; U72872; AAB17091.1; -; Genomic_DNA.
 CC HSSP; P41159; IAX8.
 CC SNR; Q95189; 3-146.
 CC InterPro; IPR012351; Cytokine_4_hlx.
 CC InterPro; IPR000065; Leptin.
 CC PANTHER; PTHR11724; Leptin; 1.
 CC Pfam; PF02024; Leptin; 1.
 CC PRINTS; PR00495; LEPTIN.
 CC ProDom; PD005698; Leptin; 1.
 CC KW Obesity.
 FT DISULFID 96 146 By similarity.
 SQ SEQUENCE 146 AA; 16031 MW; 02C43BF689M4C95C CRC64;
 Query Match 97.5%; Score 712.5; DB 1; Length 146;
 Best Local Similarity 97.9%; Pred. No. 9.8e-58;
 Matches 143; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 59
 DB 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSQKVTGLDFIPGLHPILTLKMDQTLAV 60
 QY 60 YQILTSMPSRNVQISNDLENRLDLHLAFSKSCHLPWASGLETLDSIGGVLEASGYS 119
 DB 61 YQILTSMPSRNVQISNDLENRLDLHLAFSKSCHLPWASGLETLDSIGGVLEASGYS 120
 QY 120 TEVVALSRQSGSLQDMLWQLDLSGPC 145
 DB 121 TEVVALSRQSGSLQDMLWQLDLSGPC 146
 RESULT 5
 OB_PONPY OB_PONPY STANDARD; PRT; 146 AA.
 ID OB_PONPY
 AC Q95234;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leptin (Obesity factor).
 GN Names=LEP; Synonyms=OB;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
 RT "Cloning of obese genes from different species: a comparison of the
 RT gene structures and the sequences of the obese gene products,
 RT leptin."
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- SIMILARITY: Belongs to the leptin family.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; U72873; AAB17092.1; -; Genomic_DNA.
 CC HSSP; P41159; IAX8.
 CC SNR; Q95234; 3-146.
 CC InterPro; IPR012351; Cytokine_4_hlx.
 CC InterPro; IPR000065; Leptin.
 CC PANTHER; PTHR11724; Leptin; 1.
 CC Pfam; PF02024; Leptin; 1.
 CC PRINTS; PR00495; LEPTIN.
 CC ProDom; PD005698; Leptin; 1.
 CC KW Obesity.
 FT DISULFID 96 146 By similarity.
 SQ SEQUENCE 146 AA; 16195 MW; 3F50A13338FFBBD4 CRC64;
 Query Match 96.5%; Score 705.5; DB 1; Length 146;
 Best Local Similarity 96.6%; Pred. No. 4.3e-57;
 Matches 141; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
 QY 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 59
 DB 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSQKVTGLDFIPGLHPILTLKMDQTLAV 60
 QY 60 YQILTSMPSRNVQISNDLENRLDLHLAFSKSCHLPWASGLETLDSIGGVLEASGYS 119

Db 61 YQILTSMPNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLTDLRLGGLVLEASGYS 120
 QY 120 TEVVLSRLQSGSLQDMLWQLDLSFGC 145
 Db 121 TEVVLSRLQSGSLQDMLWQLDLSFGC 146

RESULT 6
 OB_MACMU ID OB_MACMU STANDARD; PRT; 167 AA.
 AC Q28504;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=LEP; Synonyms=OB;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 NUCLEOTIDE SEQUENCE.
 RP TISSUE=Adipose tissue;
 RC MDLINE=96411743; PubMed=8810296; DOI=10.1074/jbc.271.41.25327;
 RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Nicolson M.A.,
 Hansen B.C.;
 RT "Regulation of obese (ob) mRNA and plasma leptin levels in rhesus
 monkeys. Effects of insulin, body weight, and non-insulin-dependent
 diabetes mellitus."
 RL J. Biol. Chem. 271:25327-25331(1996).
 CC -|- FUNCTION: May function as part of a signaling pathway that acts to
 regulate the size of the body fat depot. An increase in the level
 of LEP may act directly or indirectly on the CNS to inhibit food
 intake and/or regulate energy expenditure as part of a homeostatic
 mechanism to maintain constancy of the adipose mass.
 CC -|- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -|- SIMILARITY: Belongs to the leptin family.

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 removed.

 CC EMBL; U58492; AAC50730.1; -; mRNA.
 DR HSP; P41159; IAX8.
 DR SMR; Q28504; 24-167.
 DR InterPro; IPR012351; Cytokine 4_hlx.
 DR InterPro; IPR000065; Leptin.
 DR PANTHER; PTHR11724; Leptin; 1.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 DR Obesity; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 SQ SEQUENCE 167 AA; 18953 MW; E7D9F30628A5BBE9 CRC64;

Query Match 89.8%; Score 656.5; DB 1; Length 167;
 Best Local Similarity 90.4%; Pred. No. 1.7e-52;
 Matches 132; Conservative 8; Mismatches 5; Indels 1; Gaps 1;

QY 1 VPIQVQDDTKLTIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 59
 Db 22 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAI 81
 QY 60 YQILTSMPNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLTDLRLGGLVLEASGYS 119
 Db 82 YQILINLPSNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLTDLRLGGLVLEASGYS 141
 QY 120 TEVVLSRLQSGSLQDMLWQLDLSFGC 145

Db 142 TEVVLSRLQSGSLQDMLWQLDLSFGC 167

RESULT 7
 OB_FELCA ID OB_FELCA STANDARD; PRT; 167 AA.
 AC Q282C1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=LEP; Synonyms=OB;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Laurasiatheria; Carnivora; Fissipedia; Felidae;
 OC Felinae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 NUCLEOTIDE SEQUENCE.
 RP TISSUE=White adipose tissue;
 RC Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;
 RT "Molecular cloning of feline leptin cDNA".
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -|- FUNCTION: May function as part of a signaling pathway that acts to
 regulate the size of the body fat depot. An increase in the level
 of LEP may act directly or indirectly on the CNS to inhibit food
 intake and/or regulate energy expenditure as part of a homeostatic
 mechanism to maintain constancy of the adipose mass (By
 similarity).
 CC -|- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -|- SIMILARITY: Belongs to the leptin family.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

 CC EMBL; AB041360; BAA95481.1; -; mRNA.
 DR HSP; P41159; IAX8.
 DR SMR; Q282C1; 24-167.
 DR InterPro; IPR012351; Cytokine 4_hlx.
 DR InterPro; IPR000065; Leptin.
 DR PANTHER; PTHR11724; Leptin; 1.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 DR Obesity; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 SQ SEQUENCE 167 AA; 18584 MW; 643720DBB0A84B95 CRC64;

Query Match 85.3%; Score 623.5; DB 1; Length 167;
 Best Local Similarity 85.6%; Pred. No. 1.9e-49;
 Matches 125; Conservative 11; Mismatches 9; Indels 1; Gaps 1;

QY 1 VPIQVQDDTKLTIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 59
 Db 22 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAI 81
 QY 60 YQILTSMPNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLTDLRLGGLVLEASGYS 119
 Db 82 YQILINLPSNRNVQISNDLENRLDLHLVAFSKSCHLPWASGLTDLRLGGLVLEASGYS 141
 QY 120 TEVVLSRLQSGSLQDMLWQLDLSFGC 145

Db 142 TEVVLSRLQSGSLQDMLWQLDLSFGC 167
 RESULT 8
 Q6T8R8_BUBBU


```

ID Q6T8R8_BUBBU PRELIMINARY; PRT; 146 AA.
AC Q6T8R8;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Leptin (fragment).
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adipose tissue;
RA Rajendran S., Shukla D.C., Saravanan B.C.;
RT "Cloning and sequencing of buffalo leptin gene.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY427959; AK05862.1; -, mRNA.
DR HSSP; P41159; 1AX8.
DR SMR; Q6T8R8; 3-146.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
FT CHAIN <1 146 leptin.
FT NON_TER 1
SQ SEQUENCE 146 AA; 16069 MW; 1A745EE0851BD8CA CRC64;

Query Match 83.8%; Score 612.5; DB 2; Length 146;
Best Local Similarity 86.3%; Pred. No. 1.7e-48;
Matches 126; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 1 VPIQKVDPTKLIKTIYTRINDISHT-SVSSKQKVTGLDFIPGLHPILTSKMDQTLAV 59
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VPRIKVDPTKLIKTIYTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSKMDQTLAI 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 YQOILTSMSRNVIOISNDLENRLDLHLVAFKSCPLPWASGLETLDSLGGVLEASGVY 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YQOILTSLSRNVVQISNDLENRLDLHLVAFKSCPLPQVRALESLSLGGVLEASLYS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 120 TEVVALSRQGSQDMLWLQDLSPGC 145
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TEVVALSRQGSQDMLRQLDLSPGC 146
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
OB_BOVIN STANDARD; PRT; 167 AA.
AC P50595; O97918; Q95133; Q9TS29;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB, OBS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Tellam R.L., Briscoe S., Vuocolo A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE OF 22-167.
RA Ji S., Spurlock M.E.;
RT "Partial cloning of bovine obesity gene.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 22-167.
RC TISSUE=White adipose tissue;
RA Kawakita Y., Abe H., Miyashige T.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS CYS-25 AND VAL-80.
RC STRAIN=Jersey;
RX MEDLINE=20063685; PubMed=10594237; DOI=10.1007/s003359901180;
RT Konfortov B.A., Licence V.E., Miller J.R.;
RT Resequencing of DNA from a diverse panel of cattle reveals a high
RT level of polymorphism in both intron and exon.";
RN Mamm. Genome 10:1142-1145(1999).
RN [5]
RP NUCLEOTIDE SEQUENCE, AND VARIANT CYS-25.
RA Liefers S.C.;
RT "Genotype effects of bovine leptin mutations on pre- and postpartum
RT leptin concentrations.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE OF 46-145.
RA Lien S., Sundvold H., Klungland H., Vaegre D.I.;
RT "Two novel polymorphisms in the bovine obesity gene (OBS).";
RL Anim. Genet. 28:245-245(1997).
RN [7]
RP NUCLEOTIDE SEQUENCE OF 60-146.
RX MEDLINE=96269621; PubMed=8661738; DOI=10.1007/s003359900118;
RA Pfister-Genskow M.A., Hayes H., Eggen A., Bishop M.D.;
RT "Chromosomal localization of the bovine obesity (OBS) gene.";
RN Mamm. Genome 7:398-399(1996).
RN [8]
RP NUCLEOTIDE SEQUENCE OF 1-48.
RA Fitzsimmons C.J., Schmutz S.M.;
RT "Exon two of the bovine obese, leptin, gene.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U43943; AAA85906.1; -, mRNA.
DR EMBL; U50365; AAB61244.1; -, Genomic_DNA.
DR EMBL; U65793; AAB06579.1; -, mRNA.
DR EMBL; AB003143; BAA19750.1; -, mRNA.
DR EMBL; AJ132764; CAB64255.1; -, Genomic_DNA.
DR EMBL; AJ236854; CAB38018.1; -, Genomic_DNA.
DR EMBL; AJ512638; CAD54745.1; -, Genomic_DNA.
DR EMBL; AJ512639; CAD54745.1; JOINED; Genomic_DNA.
DR EMBL; Y11369; CAA72197.1; -, Genomic_DNA.
DR EMBL; U43833; AAB18762.1; -, Genomic_DNA.
DR EMBL; AF120500; AAD23567.1; -, Genomic_DNA.
DR HSSP; P41159; 1AX8.
DR SMR; P50595; 24-167.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR PANTHER; PTHR11724; Leptin; 1.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity; Polymorphism; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT VARIANT 25 25 R -> C.
FT VARIANT 80 80 A -> V.

```


FT CONFLICT 25 25 R -> Q (in Ref. 2).
 FT CONFLICT 166 166 G -> E (in Ref. 2).
 SQ SEQUENCE 167 AA; 18716 MW; 94C666B3069E50B7 CRC64;

Query Match 83.8%; Score 612.5; DB 1; Length 167;
 Best Local Similarity 86.3%; Pred. No. 2e-48; Indels 1; Gaps 1;
 Matches 126; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

Qy 1 VPIQKQVDDTKTLIKITIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
 Db 22 VPIKQVDDTKTLIKITIVTRINDISHTQSVSSKQKRVGTGLDFIPGLHPILTLTKMDQTLAI 81
 Qy 60 YQILTSPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSLGGVLEASGYS 119
 Db 82 YQILTSLPSRVVQISNDLENLRLDLHLVAFSKSCHLPQVRALESLSLGGVLEASLYS 141
 Qy 120 TEVVALSRQSGSLQDMLWQLDLSGCG 145
 Db 142 TEVVALSRQSGSLQDMLWQLDLSGCG 167

RESULT 10
 OB_BUBBU
 ID OB_BUBBU STANDARD; PRT; 167 AA.
 AC Q5J732;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=LEP; Synonyms=OB;
 OS Bubalus bubalis (Domestic water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bubalus.
 OC NCBI_TaxID=89462;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA PubMed=15566470; DOI=10.1111/j.1365-2052.2004.01186.x;
 RA Vallinoto M., Schneider M.P., Silva A., Iannuzzi L., Brenig B.;
 RT "Molecular cloning and analysis of the swamp and river buffalo leptin gene.";
 RL Anim. Genet. 35:462-463 (2004).
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- SIMILARITY: Belongs to the leptin family.
 CC -----
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 CC -----
 DR EMBL; AY495587; AAC86311.1; -; Genomic_DNA.
 DR SMR; Q5J732; 24-167.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000065; Leptin.
 DR PANTHER; PTHR11724; Leptin; 1.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PRK0495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 DR Obesity; Signal.
 KW Obesit; Signal.
 FT CHAIN 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 SQ SEQUENCE 167 AA; 18688 MW; 8524749CD69CND99 CRC64;

Query Match 83.8%; Score 612.5; DB 1; Length 167;
 Best Local Similarity 86.3%; Pred. No. 2e-48;

Matches 126; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
 Qy 1 VPIQKQVDDTKTLIKITIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
 Db 22 VPIKQVDDTKTLIKITIVTRINDISHTQSVSSKQKRVGTGLDFIPGLHPILTLTKMDQTLAI 81
 Qy 60 YQILTSPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSLGGVLEASGYS 119
 Db 82 YQILTSLPSRVVQISNDLENLRLDLHLVAFSKSCHLPQVRALESLSLGGVLEASLYS 141
 Qy 120 TEVVALSRQSGSLQDMLWQLDLSGCG 145
 Db 142 TEVVALSRQSGSLQDMLWQLDLSGCG 167

RESULT 11
 OB_PIG
 ID OB_PIG STANDARD; PRT; 167 AA.
 AC Q29406; O19095; Q95251;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=LEP; Synonyms=OB, OBS;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Adipose tissue;
 RA Louis C.F.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Ramsay T.G., Yan X.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Landrace;
 RA Robert C., Palin M.-F., Coulombe N., Roberge C., Silversides F.G., Benkel B.F., McKay R.M., Pelletier G.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Bidwell C.A., Ji S., Spurlock M.E.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Meishan;
 RA Dai R., Li N., Hu X., Wu C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RA McNeel R.L., Mersmann H.J.;
 RT "Adipose tissue regulatory transcript expression in lean versus obese pigs";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Large white;
 RA Soares M.A.M., Euclydes R.F., Guimaraes S.E.F., Martins M.F., RA Lopes P.S.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP NUCLEOTIDE SEQUENCE OF 15-110.
 RC TISSUE=White adipose tissue;
 RX MEDLINE=97009821; PubMed=8856925;
 RA Neuenchwander S., Rettenberger G., Meijerink E., Jorg H., RA Stranzinger G.;
 RT "Partial characterization of porcine obesity gene (OBS) and its localization to chromosome 18 by somatic cell hybrids.";

CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
DR EMBL; U84247; ABA1786.1; -; mRNA.
DR EMBL; U62123; AAB51033.1; -; mRNA.
DR HSSP; P41159; IAX8.
DR SMR; Q28603; 3-146.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR PANTHER; PTHR11724; Leptin; 1.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID 96 146 By similarity.
FT CONFLICT 65 65 L -> H (in Ref. 2).
FT CONFLICT 92 92 A -> G (in Ref. 2).
FT CONFLICT 124 124 V -> L (in Ref. 2).
SQ SEQUENCE 146 AA; 16054 MW; 19D54C53240968CA CRC64;

Query Match 83.2%; Score 608.5; DB 1; Length 146;
Best Local Similarity 86.3%; Pred. No. 3.9e-48;
Matches 126; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

Qy 1 VPIQVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTSLKMDQTLLAV 59
Db 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSLKMDQTLLAI 60
Qy 60 YQOILTSMPNRNVQISNDLENRLDLHLVAFSKCHLPWASGLTDLSDGVLASGYS 119
Db 61 YQOILASLPNRNVQISNDLENRLDLHLVAFSKCHLPQVRALESLSLGVLEASLYS 120
Qy 120 TEVALSRLQSLQDMLWQLDLSPEC 145
Db 121 TEVALSRLQSLQDMLWQLDLSPEC 146

RESULT 14

Q5EAE4_BOVIN PRELIMINARY; PRT; 167 AA.
AC Q5EAE4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Leptin.
GN Name=LEP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Smith T.P.L., Grosse W.M., Ersking B.A., Roberts A.J., Stone R.T.,
RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
RA Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keele J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
RT libraries and construction of a gene index for cattle.";
RL Genome Res. 11:626-630(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RA Hathay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W.,
RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
RT "Sequencing and analysis of Bos taurus full-length insert cDNA
RT clones.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; BT020625; AAX08642.1; -; mRNA.

DR SMR; Q5EAE4; 24-167.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
SQ SEQUENCE 167 AA; 18663 MW; C9AA16B31AF229CE CRC64;

Query Match 83.2%; Score 608.5; DB 2; Length 167;
Best Local Similarity 86.3%; Pred. No. 4.6e-48;
Matches 126; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

Qy 1 VPIQVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTSLKMDQTLLAV 59
Db 22 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSLKMDQTLLAI 81
Qy 60 YQOILTSMPNRNVQISNDLENRLDLHLVAFSKCHLPWASGLTDLSDGVLASGYS 119
Db 82 YQOILTSMPNRNVQISNDLENRLDLHLVAFSKCHLPQVRALESLSLGVLEASLYS 141
Qy 120 TEVALSRLQSLQDMLWQLDLSPEC 145
Db 142 TEVALSRLQSLQDMLWQLDLSPEC 167

RESULT 15

Q4VW71_CTEID PRELIMINARY; PRT; 146 AA.
AC Q4VW71;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Obese protein (Fragment).
OS Ctenopharyngodon idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=mesenteric adipose tissue;
RA Dai H., Long L.;
RT "Molecular cloning and sequence analysis of the obese gene from the
RT Ctenopharyngodon idellus.";
EL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY551335; AAT45394.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 146 AA; 16004 MW; 60D1A3BF6EB062AB CRC64;
Query Match 82.6%; Score 603.5; DB 2; Length 146;
Best Local Similarity 84.2%; Pred. No. 1.1e-47;
Matches 123; Conservative 13; Mismatches 9; Indels 1; Gaps 1;

Qy 1 VPIQVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTSLKMDQTLLAV 59
Db 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSLKMDQTLLAV 60
Qy 60 YQOILTSMPNRNVQISNDLENRLDLHLVAFSKCHLPWASGLTDLSDGVLASGYS 119
Db 61 YQOVLTSLPNQVLQINDLENRLDLHLVAFSKCHLPQVRALESLSLGVLEASLYS 120
Qy 120 TEVALSRLQSLQDMLWQLDLSPEC 145
Db 121 TEVALSRLQSLQDMLWQLDLSPEC 146

Search completed: May 4, 2006, 21:57:12
Job time : 145.502 secs

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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:52:45 ; Search time 32.8866 Seconds
(without alignments)
364.525 Million cell updates/sec

Title: US-10-623-189-2
Perfect score: 731
Sequence: 1 VPIQKVQDDTKTLIKTIVTR.....SRLQGSIQDMLWLDLSPGC 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	731	100.0	166	1	US-08-347-563A-6
2	731	100.0	166	2	US-08-292-345B-6
3	731	100.0	166	2	US-08-485-942A-6
4	731	100.0	166	2	US-08-488-214A-6
5	731	100.0	166	2	US-08-488-208A-6
6	731	100.0	166	2	US-08-483-211A-6
7	731	100.0	166	2	US-08-488-223A-6
8	731	100.0	166	2	US-08-438-431A-6
9	731	100.0	166	2	US-08-488-225A-6
10	731	100.0	166	2	US-09-204-730B-6
11	731	100.0	166	2	US-09-316-393-6
12	731	100.0	166	2	US-09-686-647A-6
13	720.5	98.6	146	1	US-08-398-021-3
14	720.5	98.6	146	1	US-08-788-943A-1
15	720.5	98.6	146	1	US-08-788-943A-4
16	720.5	98.6	146	1	US-08-788-943A-5
17	720.5	98.6	146	1	US-08-823-104-3
18	720.5	98.6	146	1	US-08-823-104-5
19	720.5	98.6	146	1	US-08-804-668-1
20	720.5	98.6	146	1	US-09-003-081-6
21	720.5	98.6	146	2	US-08-648-262-6
22	720.5	98.6	146	2	US-08-648-263-6
23	720.5	98.6	146	2	US-08-674-77A-4
24	720.5	98.6	146	2	US-08-914-375C-32
25	720.5	98.6	146	2	US-09-172-644-1
26	720.5	98.6	146	2	US-09-221-178-1
27	720.5	98.6	146	2	US-09-200-919-1

28	720.5	98.6	146	4	PCT-US96-00952-2	Sequence 2, Appli
29	720.5	98.6	146	4	PCT-US96-00952-3	Sequence 3, Appli
30	720.5	98.6	147	2	US-09-200-919-4	Sequence 4, Appli
31	720.5	98.6	148	1	US-08-429-362-3	Sequence 3, Appli
32	720.5	98.6	148	1	US-08-823-104-18	Sequence 18, Appli
33	720.5	98.6	167	1	US-08-540-242A-4	Sequence 4, Appli
34	720.5	98.6	167	1	US-08-347-563A-4	Sequence 4, Appli
35	720.5	98.6	167	1	US-09-003-081-5	Sequence 5, Appli
36	720.5	98.6	167	2	US-08-292-345B-4	Sequence 4, Appli
37	720.5	98.6	167	2	US-08-648-262-5	Sequence 5, Appli
38	720.5	98.6	167	2	US-08-648-263-5	Sequence 5, Appli
39	720.5	98.6	167	2	US-08-485-942A-4	Sequence 4, Appli
40	720.5	98.6	167	2	US-08-488-214A-4	Sequence 4, Appli
41	720.5	98.6	167	2	US-08-488-208A-4	Sequence 4, Appli
42	720.5	98.6	167	2	US-08-759-628-1	Sequence 1, Appli
43	720.5	98.6	167	2	US-08-688-908-7	Sequence 7, Appli
44	720.5	98.6	167	2	US-08-483-211A-4	Sequence 4, Appli
45	720.5	98.6	167	2	US-08-488-223A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-347-563A-6
; Sequence 6, Application US/08347563A
; Patent No. 5935810
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF INVENTIONS: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,563A
; FILING DATE: No. 5935810ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-347-563A-6

Query Match 100.0%; Score 731; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;

Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 81
Qy 61 QQLTSMPSNRVQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 120
Db 82 QQLTSMPSNRVQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 141
Qy 121 EVVALSRLOGSLQDMLWQLDLSGPC 145
Db 142 EVVALSRLOGSLQDMLWQLDLSGPC 166

RESULT 2

US-08-292-345B-6
; Sequence 6, Application US/08292345B
; Patent No. 6001968
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,345B
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Ob protein harboring Gln deletion at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-292-345B-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 81
Qy 61 QQLTSMPSNRVQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 120
Db 82 QQLTSMPSNRVQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 141
Qy 121 EVVALSRLOGSLQDMLWQLDLSGPC 145
Db 142 EVVALSRLOGSLQDMLWQLDLSGPC 166

Db 142 EVVALSRLOGSLQDMLWQLDLSGPC 166

RESULT 3

US-08-485-942A-6
; Sequence 6, Application US/08485942A
; Patent No. 6048837
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
; MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURL
; TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS
; AMENDED)
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,942A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6048837ember 30, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position
; DESCRIPTION: 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-485-942A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVY 81
Qy 61 QQLTSMPSNRVQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 120
Db 82 QQLTSMPSNRVQISNDLENRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 141

QY 121 EVVALSRLOGSLQDMLWQLDLSFGC 145
|
Db 142 EVVALSRLOGSLQDMLWQLDLSFGC 166
|

RESULT 4

US-08-488-214A-6
; Sequence 6, Application US/08488214A
; Patent No. 6124439
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
; APPLICANT: MARGHERITA MARFELI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURL
; TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
; TITLE OF INVENTION: (AS AMENDED)
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,214A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6124439ember 30, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-488-214A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKQDDTKLTKITIVTRINDISHTSVSSKQKVTGLDFPGLPILTLTKMDQTLAVY 60
|
Db 22 VPIQKQDDTKLTKITIVTRINDISHTSVSSKQKVTGLDFPGLPILTLTKMDQTLAVY 81
|
QY 61 QQILTSPSRNVIOIENDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYST 120
|

Db 82 QQILTSPSRNVIOIENDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYST 141
QY 121 EVVALSRLOGSLQDMLWQLDLSFGC 145
|
Db 142 EVVALSRLOGSLQDMLWQLDLSFGC 166
|

RESULT 5

US-08-488-208A-6
; Sequence 6, Application US/08488208A
; Patent No. 6124448
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,208A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,943
; FILING DATE: June 7, 1995
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6124448ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-08-488-208A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKQDDTKLTKITIVTRINDISHTSVSSKQKVTGLDFPGLPILTLTKMDQTLAVY 60
|
Db 22 VPIQKQDDTKLTKITIVTRINDISHTSVSSKQKVTGLDFPGLPILTLTKMDQTLAVY 81
|

Qy 61 QQILTSMPNRNVIQISNDLENLRDLHLVLAFSKSLPWLASGLETLDSLGVLASGYST 120
Db 82 QQILTSMPNRNVIQISNDLENLRDLHLVLAFSKSLPWLASGLETLDSLGVLASGYST 141
Qy 121 EVVALSRLOGSLQDMLWQLDLSFGC 145
Db 142 EVVALSRLOGSLQDMLWQLDLSFGC 166

RESULT 6
US-08-483-211A-6
; Sequence 6, Application US/08483211A
; Patent No. 6309853
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/483,211A
; FILING DATE: June 7, 1995
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6309853ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-483-211A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVTKGLDFIPGLHPILTLTKMDQTLAVY 60
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVTKGLDFIPGLHPILTLTKMDQTLAVY 81
Qy 61 QQILTSMPNRNVIQISNDLENLRDLHLVLAFSKSLPWLASGLETLDSLGVLASGYST 120
Db 82 QQILTSMPNRNVIQISNDLENLRDLHLVLAFSKSLPWLASGLETLDSLGVLASGYST 141
Qy 121 EVVALSRLOGSLQDMLWQLDLSFGC 145
Db 142 EVVALSRLOGSLQDMLWQLDLSFGC 166

RESULT 7
US-08-488-223A-6
; Sequence 6, Application US/08488223A
; Patent No. 6350730
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES TH
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,223A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,943
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6350730ember 30, 1994
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-488-223A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVTKGLDFIPGLHPILTLTKMDQTLAVY 60
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVTKGLDFIPGLHPILTLTKMDQTLAVY 81

Qy 61 QQILTSMPSRNVIQISNDLENRLDLLHLAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120
Db 82 QQILTSMPSRNVIQISNDLENRLDLLHLAFSKSCHLPWASGLETLDSLGGLVLEASGYST 141
Qy 121 EVVALSRQSGSLQDMLWQLDLSGPC 145
Db 142 EVVALSRQSGSLQDMLWQLDLSGPC 166

RESULT 8
US-08-438-431A-6
; Sequence 6, Application US/08438431A
; Patent No. 6429290
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA MAPPEI,
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PR
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,431A
; FILING DATE: May 10, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6429290ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP1
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-438-431A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKQVDDTKTLTKITVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDOTLAVY 60
Db 22 VPIQKQVDDTKTLTKITVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDOTLAVY 81
Qy 61 QQILTSMPSRNVIQISNDLENRLDLLHLAFSKSCHLPWASGLETLDSLGGLVLEASGYST 120
Db 82 QQILTSMPSRNVIQISNDLENRLDLLHLAFSKSCHLPWASGLETLDSLGGLVLEASGYST 141
Qy 121 EVVALSRQSGSLQDMLWQLDLSGPC 145

Db 142 EVVALSRQSGSLQDMLWQLDLSGPC 166
RESULT 9
US-08-488-225A-6
; Sequence 6, Application US/08488225A
; Patent No. 6471956
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,225A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/483,211
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6471956ember 30, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP2J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position
; ORIGINAL SOURCE:
; ORGANISM: Human
US-08-488-225A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKQVDDTKTLTKITVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDOTLAVY 60
Db 22 VPIQKQVDDTKTLTKITVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLTKMDOTLAVY 81

Qy 61 QQILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
Db 82 QQILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYST 141
Qy 121 EVVALSRQSGSLQDMLWQLDLSGPC 145
Db 142 EVVALSRQSGSLQDMLWQLDLSGPC 166

RESULT 10

US-09-204-730B-6
; Sequence 6, Application US/09204730B
; Patent No. 6703493
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA
; TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
; (AS AMENDED)
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/204,730B
; FILING DATE: 03-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position
; ORIGINAL SOURCE:
; ORGANISM: Human
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-204-730B-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVTGLDFIPGLHPILTLSKMDQTLAVY 60
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVTGLDFIPGLHPILTLSKMDQTLAVY 81
Qy 61 QQILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
Db 82 QQILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYST 141
Qy 121 EVVALSRQSGSLQDMLWQLDLSGPC 145
Db 142 EVVALSRQSGSLQDMLWQLDLSGPC 166

RESULT 11

US-09-316-393-6
; Sequence 6, Application US/09316393
; Patent No. 6734160
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THERE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/316,393
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Ob protein harboring Gln deletion at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; US-09-316-393-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVTGLDFIPGLHPILTLSKMDQTLAVY 60
Db 22 VPIQKVQDDTKTLIKTIVTRINDISHTSVSSKKQVTGLDFIPGLHPILTLSKMDQTLAVY 81
Qy 61 QQILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYST 120
Db 82 QQILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYST 141
Qy 121 EVVALSRQSGSLQDMLWQLDLSGPC 145
Db 142 EVVALSRQSGSLQDMLWQLDLSGPC 166

RESULT 12

US-09-686-647A-6
; Sequence 6, Application US/09686647A
; Patent No. 6821945
; GENERAL INFORMATION:
; APPLICANT: The Rockefeller University
; APPLICANT: Jeffrey M. Friedman
; APPLICANT: Yiyang Zhang

APPLICANT: Ricardo Proenca
APPLICANT: Margherita Maffei
APPLICANT: Jeffrey L. Halaas
APPLICANT: Ketan Gajiwala
APPLICANT: Stephen K. Burley
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
FILE REFERENCE: 600-1-087/CIPDIVCON
CURRENT APPLICATION NUMBER: US/09/686,647A
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: 09/183,374
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 08/347,563
PRIOR FILING DATE: 1994-11-30
PRIOR APPLICATION NUMBER: 08/292,345
PRIOR FILING DATE: 1994-08-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-09-686-647A-6

Query Match 100.0%; Score 731; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1e-73;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKTIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPIILTSKMDQTLAVY 60
Db 22 VPIQKVDDTKTIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPIILTSKMDQTLAVY 81
Qy 61 QQILTSMPSRNVQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGVLASGYST 120
Db 82 QQILTSMPSRNVQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGVLASGYST 141
Qy 121 EVVALSRLOGSLQDMLWQLDLSGPC 145
Db 142 EVVALSRLOGSLQDMLWQLDLSGPC 166

RESULT 13
US-08-398-021-3
Sequence 3, Application US/08398021
Patent No. 5594101
GENERAL INFORMATION:
APPLICANT: Becker, Gerald W.
APPLICANT: Hale, John E.
APPLICANT: MacKellar J. Warren C.
TITLE OF INVENTION: ANTI-OBESITY PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,021
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Caltrider, Steven P.
REGISTRATION NUMBER: 36,467
REFERENCE/DOCKET NUMBER: X10001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-276-0757
TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-398-021-3

Query Match 98.6%; Score 720.5; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.2e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVDDTKTIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPIILTSKMDQTLAV 59
Db 1 VPIQKVDDTKTIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPIILTSKMDQTLAV 60
Qy 60 YQILTSMPSRNVQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGVLASGYST 119
Db 61 YQILTSMPSRNVQISNDLENLRLDLHLVLAFAFKSCHLPWASGLETLDSLGVLASGYST 120
Qy 120 TEVVALSRLOGSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 14
US-08-788-943A-1
Sequence 1, Application US/08788943A
Patent No. 5831017
GENERAL INFORMATION:
APPLICANT: Hoffmann, James Arthur
TITLE OF INVENTION: OBESITY PROTEIN ANALOG COMPOUNDS AND
TITLE OF INVENTION: FORMULATIONS THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,943A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Caltrider, Steven P.
REGISTRATION NUMBER: 36,467
REFERENCE/DOCKET NUMBER: X10540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0757
TELEFAX: (317) 277-1917
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 28
OTHER INFORMATION: /note="xaa at position 28 is Gln
OTHER INFORMATION: or absent;"
US-08-788-943A-1

Query Match 98.6%; Score 720.5; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.2e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVDDTKLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
DB 1 VPIQKVDDTKLIKTIIVTRINDISHTSXSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 60 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLPWASGLETTLDSIGGVLEASGYS 119
DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLPWASGLETTLDSIGGVLEASGYS 120

QY 120 TEVVALSRLQGSLODMWLQDLSPGC 145
DB 121 TEVVALSRLQGSLODMWLQDLSPGC 146

RESULT 15
US-08-788-943A-4
; Sequence 4, Application US/08788943A
; Patent No. 5831017
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, James Arthur
; TITLE OF INVENTION: OBESITY PROTEIN ANALOG COMPOUNDS AND
; TITLE OF INVENTION: FORMULATIONS THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,943A
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10540
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0757
; TELEFAX: (317) 277-1917
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 28
; OTHER INFORMATION: /note= "Xaa at position 28 is Gln
; OTHER INFORMATION: or absent,"
US-08-788-943A-4

Query Match 98.6%; Score 720.5; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.2e-72;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVDDTKLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
DB 1 VPIQKVDDTKLIKTIIVTRINDISHTSXSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 60 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLPWASGLETTLDSIGGVLEASGYS 119

DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFSKCHLPWASGLETTLDSIGGVLEASGYS 120
QY 120 TEVVALSRLQGSLODMWLQDLSPGC 145
DB 121 TEVVALSRLQGSLODMWLQDLSPGC 146

Search completed: May 4, 2006, 21:58:24
Job time : 32.8866 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 4, 2006, 21:57:29 / Search time 112.113 Seconds
(without alignments)
540.393 Million cell updates/sec

Title: US-10-623-189-2
Perfect score: 731
Sequence: 1 VPIQKQDDTKTLTKTIVTR.....SRQGSQDMLWQLDLSPGC 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	731	100.0	145	5	US-10-623-189-2
2	731	100.0	166	3	US-09-736-084-6
3	731	100.0	166	3	US-09-316-393-6
4	731	100.0	166	4	US-10-730-488-6
5	731	100.0	166	4	US-10-780-235-6
6	720.5	98.6	146	4	US-10-191-377-1
7	720.5	98.6	146	4	US-10-139-794-10
8	720.5	98.6	146	4	US-10-419-058-2
9	720.5	98.6	146	4	US-10-467-114-1
10	720.5	98.6	146	4	US-10-622-998-1
11	720.5	98.6	146	4	US-10-658-834A-211
12	720.5	98.6	146	4	US-10-468-496-1
13	720.5	98.6	146	5	US-10-872-198-127
14	720.5	98.6	146	5	US-10-623-189-1
15	720.5	98.6	146	5	US-10-502-344-22
16	720.5	98.6	146	6	US-11-021-951-127
17	720.5	98.6	167	3	US-09-736-084-4
18	720.5	98.6	167	3	US-09-928-522-7
19	720.5	98.6	167	3	US-09-789-306-3
20	720.5	98.6	167	3	US-09-804-409A-11
21	720.5	98.6	167	3	US-09-316-393-4
22	720.5	98.6	167	4	US-10-440-464-67
23	720.5	98.6	167	4	US-10-458-334-17
24	720.5	98.6	167	4	US-10-730-488-4
25	720.5	98.6	167	4	US-10-780-295-4
26	720.5	98.6	167	5	US-10-723-860-2482
27	720.5	98.6	167	5	US-10-698-510-17

28	720.5	98.6	167	5	US-10-775-180-168	Sequence 168, App
29	720.5	98.6	167	5	US-10-775-180-169	Sequence 169, App
30	720.5	98.6	167	5	US-10-775-180-170	Sequence 170, App
31	720.5	98.6	167	5	US-10-775-180-171	Sequence 171, App
32	720.5	98.6	167	5	US-10-893-315-63	Sequence 63, Appl
33	720.5	98.6	167	5	US-10-756-149-5381	Sequence 5381, Ap
34	720.5	98.6	167	5	US-10-775-204-551	Sequence 551, App
35	720.5	98.6	167	5	US-10-775-204-555	Sequence 555, App
36	720.5	98.6	167	5	US-10-775-204-557	Sequence 557, App
37	720.5	98.6	167	5	US-10-775-204-558	Sequence 558, App
38	720.5	98.6	167	5	US-11-060-291-1	Sequence 1, Appli
39	720.5	98.6	171	5	US-10-908-400A-105	Sequence 105, App
40	720.5	98.6	178	5	US-10-893-315-108	Sequence 108, App
41	720.5	98.6	374	4	US-10-679-999-15	Sequence 15, Appl
42	720.5	98.6	374	4	US-10-679-999-18	Sequence 18, Appl
43	720.5	98.6	374	6	US-11-054-085-15	Sequence 15, Appl
44	720.5	98.6	374	6	US-11-054-085-18	Sequence 18, Appl
45	720.5	98.6	379	4	US-10-679-999-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-623-189-2
; Sequence 2, Application US/10623189
; Publication No. US20050020496A1
; GENERAL INFORMATION:
; APPLICANT: DEPAOLI, Alex M.
; APPLICANT: ORAL, Elif Arioglu
; APPLICANT: TAYLOR, Simeon I.
; APPLICANT: GARG, Abhimanyu
; TITLE OF INVENTION: USE OF LEPTIN FOR TREATING HUMAN LIPOATROPHY AND METHOD OF DETE
; TITLE OF INVENTION: PREDISPOSITION TO SAID TREATMENT
; FILE REFERENCE: 54113.8005.US02
; CURRENT APPLICATION NUMBER: US/10/623,189
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 10/279,129
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 60/336,394
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Leptin Human 145 (rHu-Leptin 1-145)
US-10-623-189-2

Query Match	100.0%;	Score 731;	DB 5;	Length 145;
Best Local Similarity	100.0%;	Pred. No. 3.8e-71;	Indels 0;	Gaps 0;
Matches 145;	Conservative 0;	Mismatches 0;		
Qy	1	VPIQKQVDDTKTLTKTIVTRINDISHSVSSKQKVTGLDIFPGLHPILTLTKMDQTLAVY	60	
Db	1	VPIQKQVDDTKTLTKTIVTRINDISHSVSSKQKVTGLDIFPGLHPILTLTKMDQTLAVY	60	
Qy	61	QQILTSMPNRNVIQISNDLENLRDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST	120	
Db	61	QQILTSMPNRNVIQISNDLENLRDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYST	120	
Qy	121	EWVALSRQGSQDMLWQLDLSPGC	145	
Db	121	EWVALSRQGSQDMLWQLDLSPGC	145	

RESULT 2
US-09-736-084-6
; Sequence 6, Application US/09736084
; Patent No. US20020107211A1
; GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/736,084
FILING DATE: 13-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
APPLICATION NUMBER: 08/347,563
FILING DATE: No. US20020107211a1ember 30, 1994
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide lacking Gln at position
ORIGINAL SOURCE: Human
ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-736-084-6
Query Match 100.0%; Score 731; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.6e-71;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKOKVTGLDFIPGLHPILTLKMDQTLAVY 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKOKVTGLDFIPGLHPILTLKMDQTLAVY 81
QY 61 QQLTSMPSNRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 120
Db 82 QQLTSMPSNRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 141
QY 121 EVVALSRLOGSLQDMLWQLDLSFGC 145
Db 142 EVVALSRLOGSLQDMLWQLDLSFGC 166
RESULT 3
US-09-316-393-6
Sequence 6, Application US/09316393
Publication No. US20030040039A1
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/316,393
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Ob protein harboring Gln deletion at position 49
ORIGINAL SOURCE: Human
ORGANISM: Human
US-09-316-393-6
Query Match 100.0%; Score 731; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.6e-71;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKOKVTGLDFIPGLHPILTLKMDQTLAVY 60
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTSVSSKOKVTGLDFIPGLHPILTLKMDQTLAVY 81
QY 61 QQLTSMPSNRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 120
Db 82 QQLTSMPSNRNVIQISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYST 141
QY 121 EVVALSRLOGSLQDMLWQLDLSFGC 145
Db 142 EVVALSRLOGSLQDMLWQLDLSFGC 166
RESULT 4
US-10-730-488-6
Sequence 6, Application US/10730488
Publication No. US20040213763A1
GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND
STEPHEN K. BURLEY
TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
(AS AMENDED)
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 17-Feb-2004
; APPLICATION NUMBER: US/10/730,488
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/736,084
; FILING DATE: 13-Dec-2000
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; APPLICATION NUMBER: 08/347,563
; FILING DATE: November 30, 1994
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide lacking Gln at position
; ORIGINAL SOURCE:
; ORGANISM: Human
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
; US-10-730-488-6
;
; Query Match 100.0%; Score 731; DB 4; Length 166;
; Best Local Similarity 100.0%; Pred. No. 4.6e-71;
; Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60
; Db 22 VPIQKVDDTKTLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 81
;
; Qy 61 QQILTSMPNRVNIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYST 120
; Db 82 QQILTSMPNRVNIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYST 141
;
; Qy 121 EVVALSRLOQSLQDMLWQLDLSPCG 145
; Db 142 EVVALSRLOQSLQDMLWQLDLSPCG 166
;
; RESULT 5
; US-10-780-295-6
; Sequence 6, Application US/10780295
; Publication No. US20040214214A1
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;
;
;
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 17-Feb-2004
; APPLICATION NUMBER: US/10/780,295
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/316,393
; FILING DATE: 21-May-1999
; APPLICATION NUMBER: 08/292,345
; FILING DATE: 17-August-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Ob protein harboring Gln deletion at position 49
; ORIGINAL SOURCE:
; ORGANISM: Human
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
; US-10-780-295-6
;
; Query Match 100.0%; Score 731; DB 4; Length 166;
; Best Local Similarity 100.0%; Pred. No. 4.6e-71;
; Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 60
; Db 22 VPIQKVDDTKTLIKTIIVTRINDISHTSVSSKQKVTGLDFIPGLHPILTLKMDQTLAVY 81
;
; Qy 61 QQILTSMPNRVNIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYST 120
; Db 82 QQILTSMPNRVNIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYST 141
;
; Qy 121 EVVALSRLOQSLQDMLWQLDLSPCG 145
; Db 142 EVVALSRLOQSLQDMLWQLDLSPCG 166
;
; RESULT 6
; US-10-191-377-1
; Sequence 1, Application US/10191377
; Publication No. US20030099709A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL FOR
; SUSTAINED DELIVERY OF BIOLOGICALLY ACTIVE AGENTS
; FILE REFERENCE: A-575
; CURRENT APPLICATION NUMBER: US/10/191,377
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PPT
; ORGANISM: Human Leptin
; US-10-191-377-1
;
; Query Match 98.6%; Score 720.5; DB 4; Length 146;
; Best Local Similarity 99.3%; Pred. No. 5.3e-70;
; Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
;
; Qy 1 VPIQKVDDTKTLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 59

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APPLICANT: Ladd, David
APPLICANT: Papisov, Mikhail
TITLE OF INVENTION: PROTEIN CONJUGATES WITH A WATER-SOLUBLE BIOCOMPATIBLE, BIODEGRADABLE
TITLE OF INVENTION: POLYMER
FILE REFERENCE: A-822
CURRENT APPLICATION NUMBER: US/10/622,998
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 60/397,509
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patent in version 3.1
SEQ ID NO 1
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-10-622-998-1

Query Match 98.6%; Score 720.5; DB 4; Length 146;
Best Local Similarity 99.3%; Pred. No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 60 YQQLTSMPSNRVQISNDLENLRLDLHLVLAFLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 119
Db 61 YQQLTSMPSNRVQISNDLENLRLDLHLVLAFLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

Qy 120 TEVVALSRQSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRQSLQDMLWQLDLSGPC 146

RESULT 11
US-10-658-834A-211
Sequence 211, Application US/10658834A
Publication No. US20040132977A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Dristanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 211
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAA60470
DATABASE ENTRY DATE: 1995-01-13
US-10-658-834A-211

Query Match 98.6%; Score 720.5; DB 4; Length 146;
Best Local Similarity 99.3%; Pred. No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 60 YQQLTSMPSNRVQISNDLENLRLDLHLVLAFLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 119
Db 61 YQQLTSMPSNRVQISNDLENLRLDLHLVLAFLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

Qy 120 TEVVALSRQSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRQSLQDMLWQLDLSGPC 146

RESULT 12
US-10-468-496-1
Sequence 1, Application US/10468496
Publication No. US20040180386A1
GENERAL INFORMATION:
APPLICANT: Carr, Francis J.
APPLICANT: Carter, Graham
APPLICANT: Jones, Tim
APPLICANT: Williams, Stephen
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
FILE REFERENCE: MER-117
CURRENT APPLICATION NUMBER: US/10/468,496
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 01103954.2
PRIOR FILING DATE: 2001-02-19
PRIOR APPLICATION NUMBER: 01105777.5
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 01106538.0
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 01106536.4
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 01107012.5
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 01106899.6
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 2036
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-10-468-496-1

Query Match 98.6%; Score 720.5; DB 4; Length 146;
Best Local Similarity 99.3%; Pred. No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 59
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 60 YQQLTSMPSNRVQISNDLENLRLDLHLVLAFLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 119
Db 61 YQQLTSMPSNRVQISNDLENLRLDLHLVLAFLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

Qy 120 TEVVALSRQSLQDMLWQLDLSGPC 145
Db 121 TEVVALSRQSLQDMLWQLDLSGPC 146

RESULT 13
US-10-872-198-127
Sequence 127, Application US/10872198
Publication No. US20050002897A1
GENERAL INFORMATION:
APPLICANT: Ulrich HAUPTS
APPLICANT: Andre KOLTERMANN
APPLICANT: Andreas SCHEIDIG
APPLICANT: Christian VOETSMER
TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
FILE REFERENCE: 04156.0002U4

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; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-127

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Query Match	98.6%	Score 720.5	DB 5	Length 146
Best Local Similarity	99.3%	Pred. No. 5.3e-70		
Matches 145	Conservative 0	Mismatches 0	Indels 1	Gaps 1
Qy	1	VPIQKVDDTKTLIKTIVTRINDISHT-SVSSQKQVTGLDFPGLHPIILTSKMDQTLLAV	59	
Ddb	1	VPIQKVDDTKTLIKTIVTRINDISHTQSVSSQKQVTGLDFPGLHPIILTSKMDQTLLAV	60	
Qy	60	YQOILTSMPSRNVIOIQNLDLENRLDLHLVLAFSKSCHLPWASGLETLDSLGGVLEASGYS	119	
Ddb	61	YQOILTSMPSRNVIOIQNLDLENRLDLHLVLAFSKSCHLPWASGLETLDSLGGVLEASGYS	120	
Qy	120	TEVVALSRLOGSLQDMLWQLDLSPGC	145	
Ddb	121	TEVVALSRLOGSLQDMLWQLDLSPGC	146	

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RESULT 14
US-10-623-189-1
; Sequence 1, Application US/10623189
; Publication No. US20050020496A1
; GENERAL INFORMATION:
; APPLICANT: DEPAOLI, Alex M.
; APPLICANT: ORAL, Elif Arioglu
; APPLICANT: TAYLOR, Simeon I.
; APPLICANT: GARG, Abhimanyu
; TITLE OF INVENTION: USE OF LEPTIN FOR TREATING HUMAN LIPOATROPHY AND METHOD OF DETERM
; TITLE OF INVENTION: PREDISPOSITION TO SAID TREATMENT
; FILE REFERENCE: 54113.8005.US02
; CURRENT APPLICATION NUMBER: US/10/623,189
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 10/279,129
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 60/336,394
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Leptin Human 146 (rHu-Leptin 1-146)
US-10-623-189-1

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Query Match          98.6%; Score 720.5; DB 5; Length 146;
Best Local Similarity 99.3%; Pred. No. 5.3e-70;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 VPIQKVDQTKLITIVTRINDISHT-SVSSKQKVTGLDFPGLHPILTLRKMDQFLAV 59
|||

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Db	1	VPTQKVQDDTKTLTKITVTRINDISHTQSVSSKKQKVTGLDPI	PGLHPILTLTISKMDQTLAV	60
QY	60	YQOILTSMPGRNVIQISNDLENIRDLHLVLA	PSKXCHLPWASGLETTLDSLGVL	EASGYS 119
Db	61	YQOILTSMPGRNVIQISNDLENIRDLHLVLA	PSKXCHLPWASGLETTLDSLGVL	EASGYS 120
QY	120	TEVVALSRQGSIQDMLWQLDLSG	PC 145	
Db	121	TEVVALSRQGSIQDMLWQLDLSG	PC 146	

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RESULT 15
US-10-502-344-22
; Sequence 22, Application US/10502344
; Publication No. US20050214762A1
; GENERAL INFORMATION:
; APPLICANT: ROSS, Richard
; APPLICANT: ARTYMUK, Peter
; APPLICANT: SAYERS, Jon
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: 100042.55084US
; CURRENT APPLICATION NUMBER: US/10/502,344
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: PCT/GB03/00253
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: GB 0201679.8
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 22
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial linker
US-10-502-344-22

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	Query Match	98.6%	Score 720.5;	DB 5;	Length 146;
	Best Local Similarity 99.3%;		Pred. No. 5.3e-70;		
	Matches 145;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
QY	1	VPIQKVODDTKTLIKTIVTRINDISHT-SVSSKQKVGTGLDFPGLHPILLTSLKMDQTLAV	59		
Db	1	VPIQKVODDTKTLIKTIVTRINDISHTQSVSSKQKVGTGLDFPGLHPILLTSLKMDQTLAV	60		
QY	60	YQOILTSMPSRNVIQI.SNDLEN.RDLLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS	119		
Db	61	YQOILTSMPSRNVIQI.SNDLEN.RDLLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS	120		
QY	120	TEVVALSRLOGSIQDMLWQLDLSPGC	145		
Db	121	TEVVALSRLOGSIQDMLWQLDLSPGC	146		

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Job time : 113.113 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2006, 21:58:39 ; Search time 17.9381 Seconds
(without alignments)

374.135 Million cell updates/sec

Title: US-10-623-189-2

Perfect score: 731

Sequence: 1 VPIQKVDDTKTLKTIIVTR.....SRLOGLQDMLWQLDLSGPC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

Published Applications AA New:
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5: /SIDSS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep1.*
6: /SIDSS5/ptodata/2/pubpaa/US09_NEW_PUB.pep1.*
7: /SIDSS5/ptodata/2/pubpaa/US09_NEW_PUB.pep1.*
8: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
9: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
10: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
11: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDSS5/ptodata/2/pubpaa/US60_NEW_PUB.pep1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720.5	98.6	146	9	US-10-519-390-19
2	720.5	98.6	146	11	US-11-176-830-211
3	720.5	98.6	167	11	US-11-236-198-32
4	720.5	98.6	185	9	US-10-821-234-1384
5	720.5	98.6	397	11	US-11-192-219-47
6	718.5	98.3	146	11	US-11-176-830-666
7	718.5	98.3	146	11	US-11-176-830-672
8	718.5	98.3	146	11	US-11-176-830-677
9	718.5	98.3	146	11	US-11-176-830-683
10	717.5	98.2	146	11	US-11-176-830-665
11	717.5	98.2	146	11	US-11-176-830-671
12	717.5	98.2	146	11	US-11-176-830-673
13	717.5	98.2	146	11	US-11-176-830-676
14	717.5	98.2	146	11	US-11-176-830-682
15	717.5	98.2	146	11	US-11-236-198-36
16	715.5	97.9	146	11	US-11-176-830-674
17	715.5	97.9	146	11	US-11-176-830-675
18	715.5	97.9	146	11	US-11-176-830-679
19	715.5	97.9	146	11	US-11-176-830-681
20	714.5	97.7	146	11	US-11-176-830-678
21	714.5	97.7	146	11	US-11-176-830-680

22	712.5	97.5	146	11	US-11-176-830-663	Sequence 663, App
23	712.5	97.5	146	11	US-11-176-830-664	Sequence 664, App
24	712.5	97.5	146	11	US-11-176-830-667	Sequence 667, App
25	712.5	97.5	146	11	US-11-176-830-668	Sequence 668, App
26	712.5	97.5	146	11	US-11-236-198-31	Sequence 31, Appl
27	711.5	97.3	146	9	US-10-926-798-5	Sequence 5, Appli
28	707.5	96.8	146	11	US-11-176-830-670	Sequence 670, App
29	706.5	96.6	146	11	US-11-176-830-669	Sequence 669, App
30	705.5	96.5	146	11	US-11-236-198-37	Sequence 37, Appl
31	656.5	89.8	167	11	US-11-236-198-33	Sequence 33, Appl
32	612.5	83.8	167	11	US-11-236-198-28	Sequence 28, Appl
33	611.5	83.7	167	11	US-11-236-198-39	Sequence 39, Appl
34	608.5	83.2	146	11	US-11-236-198-35	Sequence 35, Appl
35	603.5	82.6	167	11	US-11-236-198-34	Sequence 34, Appl
36	597	81.7	163	11	US-11-236-198-30	Sequence 30, Appl
37	592.5	81.1	178	9	US-10-926-798-8	Sequence 8, Appli
38	589.5	80.6	167	11	US-11-236-198-38	Sequence 38, Appl
39	587.5	80.4	178	9	US-10-926-798-15	Sequence 15, Appl
40	585.5	80.1	178	9	US-10-926-798-16	Sequence 16, Appl
41	584.5	80.0	178	9	US-10-926-798-17	Sequence 17, Appl
42	583.5	79.8	146	11	US-11-236-198-29	Sequence 29, Appl
43	138.5	18.9	32	9	US-10-841-218-1	Sequence 1, Appli
44	125	17.1	26	9	US-10-841-218-2	Sequence 2, Appli
45	120	16.4	22	11	US-11-236-198-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1

US-10-519-390-19
Sequence 19, Application US/10519390
Publication No. US2006008872A1
GENERAL INFORMATION:
APPLICANT: MEDEXGEN Inc.
APPLICANT: CHUNG, Yong-Hoon
APPLICANT: LEE, Hak-sup
APPLICANT: YI, Ki-Wan
APPLICANT: KIM, Jae-Youn
APPLICANT: HEO, Youn-Hwa
TITLE OF INVENTION: A method of improving efficacy of biological response-modifying
TITLE OF INVENTION: proteins and the example mutants
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/519,390
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: KR10-2003-0051846
PRIOR FILING DATE: 2003-07-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Kopatentin 1.71
SEQ ID NO 19
LENGTH: 146
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: LPT: 41st or 92nd Phe is replaced by Val.
US-10-519-390-19

Query Match	98.6%	Score	720.5	DB	9	Length	146
Best Local Similarity	99.3%	Pred. No.	1.6e-64	Indels	1	Gaps	1
Matches	145	Conservative	0	Mismatches	0		
Qy	1	VPIQKVDDTKTLKTIIVTRINDISHT-SVSSSKOKVTGLDFIPGLHPILTLSKMDQTLAV	59				
Db	1	VPIQKVDDTKTLKTIIVTRINDISHTQSVSSKQKVGLDFIPGLHPILTLSKMDQTLAV	60				
Qy	60	YQQLTSMPSRNVQISNDLENLDLHLVAFSCKLHPWASGLETLDLGGVLEASGYS	119				
Db	61	YQQLTSMPSRNVQISNDLENLDLHLVAFSCKLHPWASGLETLDLGGVLEASGYS	120				
Qy	120	TEVVALSRLOGLQDMLWQLDLSGPC	145				
Db	121	TEVVALSRLOGLQDMLWQLDLSGPC	146				

```
RESULT 2
US-11-176-830-211
; Sequence 211, Application US/11176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; FILE OF INVENTION: Acid Molecules and Related Applications
; FILE REFERENCE: 17109-012002 (922B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAA60470
; DATABASE ENTRY DATE: 1995-01-13
US-11-176-830-211

Query Match      98.6%; Score 720.5; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.6e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
      |||
Db      1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY      60 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDLSLGGVLEASGYS 119
      |||
Db      61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDLSLGGVLEASGYS 120

QY      120 TEVVALSRQGSLOQMLWQDLSPGC 145
      |||
Db      121 TEVVALSRQGSLOQMLWQDLSPGC 146

RESULT 3
US-11-236-198-32
; Sequence 32, Application US/11236198
; Publication No. US20060030530A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Fruebis, Joachim
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
; FILE REFERENCE: 70 US2 REG
; CURRENT APPLICATION NUMBER: US/11/236,198
; CURRENT FILING DATE: 2005-09-27
; PRIOR APPLICATION NUMBER: US/09/668,558
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,506
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent.pm
; SEQ ID NO 32
; LENGTH: 167
; TYPE: PRT

Query Match      98.6%; Score 720.5; DB 11; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.6e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
      |||
Db      1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY      60 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDLSLGGVLEASGYS 119
      |||
Db      61 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDLSLGGVLEASGYS 120

QY      120 TEVVALSRQGSLOQMLWQDLSPGC 145
      |||
Db      121 TEVVALSRQGSLOQMLWQDLSPGC 146

RESULT 4
US-10-821-234-1384
; Sequence 1384, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1384
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1384

Query Match      98.6%; Score 720.5; DB 9; Length 185;
Best Local Similarity 99.3%; Pred. No. 2.2e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
      |||
Db      40 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 99

QY      60 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDLSLGGVLEASGYS 119
      |||
Db      100 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDLSLGGVLEASGYS 159

QY      120 TEVVALSRQGSLOQMLWQDLSPGC 145
      |||
Db      160 TEVVALSRQGSLOQMLWQDLSPGC 185

RESULT 5
US-11-192-219-47
; Sequence 47, Application US/11192219
; Publication No. US20050272656A1
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; TITLE OF INVENTION: USES FOR WSX LIGANDS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
```

```
; ORGANISM: Homo sapiens
US-11-236-198-32

Query Match      98.6%; Score 720.5; DB 11; Length 167;
Best Local Similarity 99.3%; Pred. No. 2e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
      |||
Db      22 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY      60 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDLSLGGVLEASGYS 119
      |||
Db      82 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDLSLGGVLEASGYS 141

QY      120 TEVVALSRQGSLOQMLWQDLSPGC 145
      |||
Db      142 TEVVALSRQGSLOQMLWQDLSPGC 167

RESULT 4
US-10-821-234-1384
; Sequence 1384, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1384
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1384

Query Match      98.6%; Score 720.5; DB 9; Length 185;
Best Local Similarity 99.3%; Pred. No. 2.2e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 VPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
      |||
Db      40 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 99

QY      60 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDLSLGGVLEASGYS 119
      |||
Db      100 YQOILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLPWASGLETLDLSLGGVLEASGYS 159

QY      120 TEVVALSRQGSLOQMLWQDLSPGC 145
      |||
Db      160 TEVVALSRQGSLOQMLWQDLSPGC 185

RESULT 5
US-11-192-219-47
; Sequence 47, Application US/11192219
; Publication No. US20050272656A1
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; TITLE OF INVENTION: USES FOR WSX LIGANDS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
```

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/192,219
FILING DATE: 27-Jul-2005
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/667,197
FILING DATE: 20-Jun-1996
APPLICATION NUMBER: 08/585005
FILING DATE: 08-Jan-96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: P-40,378
REFERENCE/DOCKET NUMBER: P0986P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-11-192-219-47

Query Match 98.6%; Score 720.5; DB 11; Length 397;
Best Local Similarity 99.3%; Pred.No. 6.1e-64; Indels 1; Gaps 1;
Matches 145; Conservative 0; Mismatches 0;
QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
DB 22 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
QY 60 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 119
DB 82 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 141
QY 120 TEVVALSRQSLQDMLWQLDLSGPC 145
DB 142 TEVVALSRQSLQDMLWQLDLSGPC 167

RESULT 6
US-11-176-830-666
Query Match 98.6%; Score 718.5; DB 11; Length 146;
Best Local Similarity 99.6%; Pred.No. 2.6e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
FILE REFERENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR APPLICATION NUMBER: 10/658,834
PRIOR FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 666
LENGTH: 146

TYPE: PRT
ORGANISM: Homo sapiens
US-11-176-830-666
Query Match 98.3%; Score 718.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred.No. 2.6e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
DB 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 60 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 119
DB 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
QY 120 TEVVALSRQSLQDMLWQLDLSGPC 145
DB 121 TEVVALSRQSLQDMLWQLDLSGPC 146

RESULT 7

US-11-176-830-672
Query Match 98.3%; Score 718.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred.No. 2.6e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding
FILE REFERENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR APPLICATION NUMBER: 10/658,834
PRIOR FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 672
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-11-176-830-672

Query Match 98.3%; Score 718.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred.No. 2.6e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 59
DB 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 60 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 119
DB 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
QY 120 TEVVALSRQSLQDMLWQLDLSGPC 145
DB 121 TEVVALSRQSLQDMLWQLDLSGPC 146

RESULT 8

US-11-176-830-677
Query Match 98.3%; Score 718.5; DB 11; Length 146;
Best Local Similarity 98.6%; Pred.No. 2.6e-64;
Matches 144; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry

```

: APPLICANT: Dristanti, Lila
: APPLICANT: Vega, Manuel
: TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
: TITLE OF INVENTION: Acid Molecules and Related Applications
: FILE REFERENCE: 17109-012002 (922B)
: CURRENT APPLICATION NUMBER: US/11/176.830
: CURRENT FILING DATE: 2005-07-06
: PRIOR APPLICATION NUMBER: 10/658,834
: PRIOR FILING DATE: 2003-09-08
: PRIOR APPLICATION NUMBER: 60/457,135
: PRIOR FILING DATE: 2003-03-21
: PRIOR APPLICATION NUMBER: 60/409,898
: PRIOR FILING DATE: 2002-09-09
: NUMBER OF SEQ ID NOS: 1306
: SOFTWARE: Fast-SEQ for Windows Version 4.0
: SEQ ID NO 677
: LENGTH: 146
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-11-176-830-677

```

Query Match	98.3%	Score 718.5;	DB 11;	Length 146;
Best Local Similarity	98.6%;	Pred. NO. 2.6e-64;		
Matches 144;	Conservative 1;	Mismatches 0;	Indels 1;	Gaps 1;
Qy	1	VPIQKVODDTKLTIKTIIVTRINDISHT--SVSSKQKVTGLDFIPGLHPILTIUSKMDQTLAV	59	
Db	1	VPIQKVODDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTIUSKMDQTLAV	60	
Qy	60	YQQLTSMPSRNVIIQISNDLENLRDLLHLVLAFAFSKSCHLPWASGLETTLDSLGVLKASGYS	119	
Db	61	YQQLTSMPSRNVIIQISNDLENLRDLLHLVLAFAFSKSCHLPWASGLETTLDSLGVLKASGYS	120	
Qy	120	TEVVALLRQGSLODMLWQLDLSFGC	145	
Db	121	TEVVALLRQGSLODMLWQLDLSFGC	146	

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RESULT 9
US-11-176-830-683
; Sequence 683, Application US/11176830
; Publication No. US20060020116A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid Molecules and Related Applications
; FILE REFERENCE: 17109-012002 (322B)
; CURRENT APPLICATION NUMBER: US/11/176,830
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 10/658,834
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 683
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-683

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	Query Match	98.3%	Score 718.5;	DB 11;	Length 146;
	Best Local Similarity	98.6%;	Pred. No. 2.66-64;		
	Matches 144;	Conservative 1;	Mismatches 0;	Indels 1;	Gaps 1;
Qy	1	VPIQKVODDTKLLIKTIWTRINDISHT-SVSSKOKVTGLDEIPGLHPILITSKMDQTLAV	59		
Db	1	VPIQKVODDTKLLIKTIWTRINDISHTCSVSSKOKVTGLDEIPGLHPILITSKMDQTLAV	60		

Qy	60	YQQLTTPSPSRNVQISNDLENLRLDLHLVLAFAFSKSCHLPWASGLETTLDSLGVLASGYS	119
Db	61	YQQLTTPSPSRNVQISNDLENLRLDLHLVLAFAFSKSCHLPWASGLETTLDSLGVLASGYS	120
Qy	120	TEVVALSRLOGSLOQDMLWQLDLSPGC	145
Db	121	TEVVALSRLOGSLOQDMLWQLDLSPGC	146

RESULT 10
 US-11-176-830-665
 ; Sequence 665, Application US/11176830
 ; Publication No. US20060020116A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gantier, Rene
 ; APPLICANT: Guyon, Thierry
 ; APPLICANT: Drittanti, Lila
 ; APPLICANT: Vega, Manuel
 ; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
 ; TITLE OF INVENTION: Acid Molecules and Related Applications
 ; FILE REFERENCE: 17109-012002 (922B)
 ; CURRENT APPLICATION NUMBER: US/11/176,830
 ; CURRENT FILING DATE: 2005-07-06
 ; PRIOR APPLICATION NUMBER: 10/658,834
 ; PRIOR FILING DATE: 2003-09-08
 ; PRIOR APPLICATION NUMBER: 60/457,135
 ; PRIOR FILING DATE: 2003-03-21
 ; PRIOR APPLICATION NUMBER: 60/409,898
 ; PRIOR FILING DATE: 2002-09-09
 ; NUMBER OF SEQ ID NOS: 1306
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 665
 ; LENGTH: 146
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-176-830-665

	Query Match	98.2%;	Score 717.5;	DB 11;	Length 146;
	Best Local Similarity	98.6%;	Pred. No. 3.2e-64;		
	Matches 144;	Conservative 1;	Mismatches 0;	Indels 1;	Gaps 1;
Qy	1	VPIQKVQDDTKLTIKTIIVTRINDISHT-SVSSKQKV7GLDFIPGLHPIILTSKMDQTLAV	59		
Db	1	VPIQKVQDDTKLTIKTIIVTRINDISHTQSVSSKQKV7GLDFIPGLHPIILTSKMDQTLAV	60		
Qy	60	YQQLTSMPSRNVIIQISNDLENLRDLDLHVLAFSSCHLPWASGLETLDLSGLGVLEASGY	119		
Db	61	YQQLTSMPSRNVIIQISNDLENLRDLDLHVLAFSSCHLPWASGLETLDLSGLGVLEASGY	120		
Qy	120	TEVVALSRLQGSIQDMLWQLDLSPGC	145		
Db	121	TEVVALSRLQGSIQDMLWQLDLSPGC	146		

RESULT 11
 US-11-176-830-671
 ; Sequence 671, Application US/11176830
 ; Publication No. US20080020116A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gantier, Rene
 ; APPLICANT: Guyon, Thierry
 ; APPLICANT: Drittanti, Lila
 ; APPLICANT: Vega, Manuel
 ; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
 ; TITLE OF INVENTION: Acid Molecules and Related Applications
 ; FILE REFERENCE: 17109-012002 (922B)
 ; CURRENT APPLICATION NUMBER: US/11/176,830
 ; CURRENT FILING DATE: 2005-07-06
 ; PRIOR APPLICATION NUMBER: 10/658,834
 ; PRIOR FILING DATE: 2003-09-08
 ; PRIOR APPLICATION NUMBER: 60/457,135
 ; PRIOR FILING DATE: 2003-03-21

